GenCore version 4.5

OM protein - protein search, using sw model

Run on: February 13, 2002, 17:37:34 ; Search time 16.12 Seconds
(without alignments)
1828.756 Million cell updates/sec

Title: US-09-550-103-1
Perfect score: 2031
Sequence: 1 MGNRSTADADGLLAGRGPAA.....YTVFNAEFRNVFRKALRACC 387

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2026	99.8	387	1	DYHUD4	dopamine receptor
2	1510	74.3	387	2	I49246	D4 dopamine recept
3	683	33.6	446	1	DYRTD3	dopamine receptor
4	679	33.4	400	2	G01977	d3 dopamine recept
5	675	33.2	400	2	G00013	D3 dopamine recept
6	669	32.9	446	2	I48322	dopamine receptor
7	658.5	32.4	514	2	D56849	dopamine receptor-
8	645	31.8	443	1	DYHUD2	dopamine receptor
9	638	31.4	511	2	C56849	dopamine receptor-
10	636.5	31.3	444	1	DYBOD2	dopamine receptor
11	631.5	31.1	444	1	DYMSD2	dopamine receptor
12	631.5	31.1	444	1	S08146	dopamine receptor
13	629.5	31.0	442	1	DYXLD2	dopamine receptor
14	581	28.6	450	2	A38316	alpha-2-adrenergic
15	574.5	28.3	450	2	A37223	alpha-2B-adrenergi
16	573	28.2	484	2	S58868	G protein-coupled
17	566	27.9	450	2	A34169	alpha-2A-adrenergi
18	565.5	27.8	461	2	A31237	alpha-2C-adrenergi
19	563.5	27.7	448	2	I51883	alpha-2B-adrenergi
20	563.5	27.7	455	2	S28221	alpha-2-C2 adrener
21	560.5	27.6	453	2	A35642	alpha-2B-adrenergi
22	559.5	27.5	379	2	JC6178	serotonin receptor
23	552	27.2	458	2	A40392	alpha-2-adrenergic
24	551	27.1	450	2	I49481	alpha-2 adrenergic
25	550	27.1	450	2	B40392	alpha-2-adrenergic
26	547.5	27.0	458	2	A48392	alpha 2C4 adrenoce
27	547.5	27.0	458	2	I49480	alpha-2 adrenergic
28	542.5	26.7	422	2	JH0315	serotonin receptor
29	542	26.7	458	2	A37869	alpha-2B-adrenergi
30	536.5	26.4	421	2	I49375	serotonin receptor
31	532.5	26.2	476	2	JC5042	G protein-coupled
32	529	26.0	601	2	S12004	tyramine receptor
33	529	26.0	601	2	JH0170	octopamine recepto
34	527	25.9	422	2	I38209	serotonin receptor
35	527	25.9	450	2	JH0190	alpha-2-adrenergic
36	522	25.7	432	2	I50829	alpha 2-adrenocept
37	512.5	25.2	480	2	I53053	beta 1 adrenergic
38	508	25.0	400	2	S32804	beta-3-adrenergic
39	504.5	24.8	564	2	A38271	serotonin receptor
40	500.5	24.6	405	2	S65459	beta-3-adrenergic
41	500.5	24.6	418	2	G02953	beta-3-adrenergic
42	498	24.5	509	2	A47174	serotonin receptor
43	497.5	24.5	408	1	QRHUBE	beta-3-adrenergic
44	497.5	24.5	414	1	QRHUB3	beta-3-adrenergic
45	495	24.4	477	1	QRHUB1	beta-1-adrenergic

ALIGNMENTS

RESULT 1
DYHUD4
dopamine receptor D4 - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 02-Sep-1997
C;Accession: S15079
R;van Tol, H.H.M.; Bunzow, J.R.; Guan, H.C.; Sunahara, R.K.; Seeman, P.; Niznik, H.B
Nature 350, 610-614, 1991
A;Title: Cloning of the gene for a human dopamine D(4) receptor with high affinity f
A;Reference number: S15079; MUID:91204054
A;Accession: S15079
A;Molecule type: DNA
A;Residues: 1-387 <VAN>
A;Cross-references: EMBL:X58497
C;Genetics:
A;Gene: GDB:DRD4
A;Cross-references: GDB:127782; OMIM:126452
A;Map position: 11p15.5-11p15.5
A;Introns: 95/3; 133/2; 269/2; 321/1
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; neurotra
F;34-60/Domain: transmembrane #status predicted <TM1>
F;72-96/Domain: transmembrane #status predicted <TM2>
F;110-131/Domain: transmembrane #status predicted <TM3>
F;153-174/Domain: transmembrane #status predicted <TM4>
F;192-214/Domain: transmembrane #status predicted <TM5>
F;215-314/Domain: intracellular #status predicted <INT>
F;315-339/Domain: transmembrane #status predicted <TM6>
F;349-368/Domain: transmembrane #status predicted <TM7>
F;3/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;108-185/Disulfide bonds: #status predicted
F;149,239/Binding site: phosphate (Ser) (covalent) #status predicted
F;297,306/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 99.8%; Score 2026; DB 1; Length 387;
Best Local Similarity 99.7%; Pred. No. 1e-122;
Matches 386; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60

Qy      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVMLCT 120

Qy     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180

Qy     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240

Qy    241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300

Qy    301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360

Qy    361 SALNPVIYTVFNAEFRNVFRKALRACC 387
          |||||||||||||||||||||||||||
Db    361 SALNPVIYTVFNAEFRNVFRKALRACC 387


RESULT   2
I49246
D4 dopamine receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: I49246
R;Fishburn, C.S.; Carmon, S.; Fuchs, S.
FEBS Lett. 361, 215-219, 1995
A;Title: Molecular cloning and characterisation of the gene encoding the murine D4 dopam
A;Reference number: I49246; MUID:95212551
A;Accession: I49246
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-387 <RES>
A;Cross-references: EMBL:U19880; NID:g758426; PIDN:AAC52190.1; PID:g758427
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor


  Query Match             74.3%;  Score 1510;  DB 2;  Length 387;
  Best Local Similarity   76.1%;  Pred. No. 1e-89;
  Matches  302;  Conservative   18;  Mismatches   57;  Indels   20;  Gaps    4;

Qy      1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
          ||| |  :  ||||||||    | |  ||| | ||||||||||||| ||||||||||||
Db      1 MGNSSATEDGGLLAGRGP---ESLGTGAGLGGAGAAALVGGVLLIGLVLAGNSLVCVSVA 57

Qy     61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
          :|| |||||| |||||||||||||:|||||||||||||| |||||||| |||||| |||
Db     58 SERTLQTPTNYFIVSLAAADLLLAVLVLPLFVYSEVQGGVWLLSPRLCDTLMAMDVMLCT 117

Qy    121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
          |||||||||||||||| ||||||:||  : ||||| ||||||||||:||:|||||| ||
Db    118 ASIFNLCAISVDRFVAVTVPLRYNQQG--QCQLLLIAATWLLSAAVASPVVCGLNDVPGR 175

Qy    181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
          ||||| ||:|||||||||||||||||||||||||||||||:||| ||  ||| ||||||||
Db    176 DPAVCCLENRDYVVYSSVCSFFLPCPLMLLLYWATFRGLRRWEAARHTKLHSRAPRRPSG 235

Qy    241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSN----------CAPPDAVRAAALP 290
          ||||   |      | |  ||| || | |   |  |:          |:|   :  ||||
Db    236 PGPPVSDP-----TQGPFFPDCPPPLPSLRTSPSDSSRPESELSQRPCSPGCLLADAALP 290

Qy    291 PQTPPQTRRRRRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLV 350
          | :|||| ||||||||||||||||||||||:||||||||||:|||||| | ||||
Db    291 QPPEPSSRRRRGAKITGRERKAMRVLPVVVGAFLVCWTPFFVVHITRALCPACFVSPRLV 350

Qy    351 SAVTWLGYVNSALNPVIYTVFNAEFRNVFRKALRACC 387
          |||||||||||||||:|||:|||||:|||| ||  |
Db    351 SAVTWLGYVNSALNPIIYTIFNAEFRSVFRKTLRLRC 387


RESULT   3
DYRTD3
dopamine receptor D3 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C;Accession: S11565; S41849; I52280
R;Sokoloff, P.; Giros, B.; Martres, M.P.; Bouthenet, M.L.; Schwartz, J.C.
Nature 347, 146-151, 1990
A;Title: Molecular cloning and characterization of a novel dopamine receptor (D(3))
A;Reference number: S11565; MUID:90370111
A;Accession: S11565
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-446 <SOK>
A;Cross-references: EMBL:X53944; NID:g56060; PIDN:CAA37887.1; PID:g56061
R;Giros, B.; Martres, M.P.; Pilon, C.; Sokoloff, P.; Schwartz, J.C.
Biochem. Biophys. Res. Commun. 176, 1584-1592, 1991
A;Title: Shorter variants of the D(3) dopamine receptor produced through various pat
A;Reference number: S41849; MUID:91248260
A;Accession: S41849
A;Molecule type: DNA
A;Residues: 1-138,'E',140-446 <GIR>
R;Pagliusi, S.; Chollet-Daemerius, A.; Losberger, C.; Mills, A.; Kawashima, E.
Biochem. Biophys. Res. Commun. 194, 465-471, 1993
A;Title: Characterization of a novel exon within the D3 receptor gene giving rise to
A;Reference number: I52280; MUID:93326159
A;Accession: I52280
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 71-106 <RES>
A;Cross-references: GB:S63847; NID:g399705; PIDN:AAB27545.1; PID:g399707
A;Experimental source: strain Wistar, brain
C;Genetics:
A;Introns: 90/3
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; lipoprotein; neurotransmitter
F;33-55/Domain: transmembrane #status predicted <TM1>
F;67-92/Domain: transmembrane #status predicted <TM2>
F;105-126/Domain: transmembrane #status predicted <TM3>
F;150-172/Domain: transmembrane #status predicted <TM4>
F;186-209/Domain: transmembrane #status predicted <TM5>
F;210-375/Domain: intracellular #status predicted <CYT>
F;376-399/Domain: transmembrane #status predicted <TM6>
F;413-434/Domain: transmembrane #status predicted <TM7>
F;12,19/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;103-181/Disulfide bonds: #status predicted
F;446/Binding site: palmitate (Cys) (covalent) #status predicted


  Query Match             33.6%;  Score 683;  DB 1;  Length 446;
  Best Local Similarity   37.4%;  Pred. No. 8.6e-37;
  Matches  154;  Conservative   54;  Mismatches  126;  Indels   78;  Gaps    8;

Qy     44 LIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLL 103
          || |:: || ||| :|  |||||| ||  :|||| ||||:| ||:|  || || || | |
Db     39 LILAIIFGNGLVCAAVLRERALQTTTNYLVVSLAVADLLVATLVMPWVVYLEVTGGVWNF 98

Qy    104 SPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYNR---QGGSRRQLLLIGATW 160
          |   ||  : :|| :||||| ||||||:||: || :|: |     |   ||  |:| | |
Db     99 SRICCDVFVTLDVMMCTASILNLCAISIDRYTAVVMPVHYQHGTGQSSCRRVALMITAVW 158

Qy    161 LLSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLY---WATFR 217
          :|: ||: |:| | |    ||::| : : |:|:|||| ||::|  : :|:|   :   |
Db    159 VLAFAVSCPLLFGFNTT--GDPSICSISNPDFVIYSSVVSFYVPFGVTVLVYARIYIVLR 216

Qy    218 GLQRWEVARRAKLHGRAPRRPSGPGPPSPT---------------------------- 247
            ||  :  |      : |    || |  :
Db    217 QRQRKRILTRQNSQCISIR----PGFPQQSSCLRLHPIRQFSIRARFLSDATGQMEHIED 272

Qy    248 PPAPRLPQDPCGPDCAPPAPGL-------------------PPDPCGSNCAPPDAVRAAA 288
          |:  |||      ||:||                      |    |:  :| : | :
Db    273 KQYPQKCQDPLLSHLQPPSPGQTHGGLKRYYSICQDTALRHPSLEGGAGMSPVERTRNSL 332

Qy    289 LPPQTPP---QTRRRRRAKITG--------------RERKAMRVLPVVVGAFLLCWTPFF 331
           |   |    : |:    :::                ||:|| ::: :|:|||::|| |||
Db    333 SPTMAPKLSLEVRKLSNGRLSTSLRLGPLQPRGVPLREKKATQMVVIVLGAFIVCWLPFF 392

Qy    332 VVHITQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKAL 383
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          : |:    | || | | |  | ||||||||||||||||| || |||  | | |
Db    393 LTHVLNTHCQACHVSPELYRATTWLGYVNSALNPVIYTTFNVEFRKAFLKIL 444


RESULT   4
G01977
d3 dopamine receptor - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 13-Aug-1999
C;Accession: G01977
R;Fishburn, C.S.; Park, B.
submitted to the EMBL Data Library, July 1995
A;Reference number: G08971
A;Accession: G01977
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-400 <FIS>
A;Cross-references: EMBL:U32499; NID:g927341; PIDN:AAA73929.1; PID:g927342
C;Superfamily: vertebrate rhodopsin


  Query Match             33.4%;  Score 679;  DB 2;  Length 400;
  Best Local Similarity   38.8%;  Pred. No. 1.4e-36;
  Matches  155;  Conservative   51;  Mismatches  141;  Indels   52;  Gaps    8;

Qy      21 GASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAAD 80
           ||     |  |   |   :    || |:: || |||::|  |||||| ||  :|||| ||
Db      16 GAENSTGASQARPHAYYALSYCALILAIVFGNGLVCMAVLKERALQTTTNYLVVSLAVAD 75

Qy      81 LLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVP 140
           ||:| ||:|  || || || |  |   ||  : :|| :||||| ||||||:||: || :|
Db      76 LLVATLVMPWVVYLEVTGGVWNFSRICCDVFVTLDVMMCTASILNLCAISIDRYTAVVMP 135

Qy     141 LRYNR---QGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSS 197
           : |     |   ||  |:| | |:|: ||: |:| | |     || || : : |:|:|||
Db     136 VHYQHGTGQSSCRRVALMITAVWVLAFAVSCPLLFGFNTT--GDPTVCSISNPDFVIYSS 193

Qy     198 VCSFFLPCPLMLLLY---WATFRGLQRWEVARRAKLHGRAPRRPSGPGPPSPTPPAPRLP 254
           | ||:||  : :|:|   :   :  :|  :  |     : |           |  |
Db     194 VVSFYLPFGVTVLVYARIYVVLKQRRRKRILTRQNSQCNSVR----------PGFP 239

Qy     255 QDPCGPD------------CAPPAPGLPP-DPCGSNCAPPDAVRAAALP---PQTPPQTR 298
           |    ||            |   | | |     |      :  | :  |   |:   : |
Db     240 QQTLSPDPAHLELKRYYSICQDTALGGPGFQERGGELKREEKTRNSLSPTIAPKLSLEVR 299

Qy     299 RRRRAKITG----------RERKAMRVLPVVVGAFLLCWTPPFVVHITQALCPACS 344
           :   :::              ||:|| ::: :|:|||::|| |||: |:    |  |
Db     300 KLSNGRLSTSLKLGPLQPRGVPLREKKATQMVAIVLGAFIVCWLPFFLTHVLNTHCQTCH 359

Qy     345 VPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKAL 383
           | | | || |||||||||||||||| || |||  | | |
Db     360 VSPELYSATTWLGYVNSALNPVIYTTFNIEFRKAFLKIL 398


RESULT   5
G00013
D3 dopamine receptor - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 13-Aug-1999
C;Accession: G00013
R;Ross, P.C.
submitted to the EMBL Data Library, February 1995
A;Reference number: G00049
A;Accession: G00013
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-400 <ROS>
A;Cross-references: EMBL:U21307; NID:g984965; PIDN:AAA75379.1; PID:g984966
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor


  Query Match             33.2%;  Score 675;  DB 2;  Length 400;
  Best Local Similarity   39.9%;  Pred. No. 2.5e-36;
  Matches  150;  Conservative   50;  Mismatches  124;  Indels   52;  Gaps    8;

Qy      44 LIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLL 103
           || |:: || |||::|  |||||| ||  :|||| ||||:| ||:|  || || || |
Db      39 LILAIVFGNGLVCMAVLKERALQTTTNYLVVSLAVADLLVATLVMPWVVYLEVTGGVWNF 98

Qy     104 SPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYNR---QGGSRRQLLLIGATW 160
           |   ||  : :|| :||||| ||||||:||: || :|: |     |   ||  |:| | |
Db      99 SRVCCDVFVTLDVMMCTASILNLCAISIDRYTAVVMPVHYQHGTGQSSCRRVTLMITAVW 158

Qy     161 LLSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLY---WATFR 217
           :|: ||: |:| | |     || || : : |:|:|||| ||:||  : :|:|   :   :
Db     159 VLAFAVSCPLLFGFNTT--GDPTVCSISNPDFVIYSSVVSFYLPFGVTVLVYARIYVVLK 216

Qy     218 GLQRWEVARRAKLHGRAPRRPSGPGPPSPTPPAPRLPQDPCGPD-----------CAPP 265
             :|  :  |     : |              |  ||   ||           |
Db     217 QRRRKRILTRQNSQCNSVR-------------PGFPQQTLSPDRAHLELKRYYSICQDT 262

Qy     266 APGLPP-DPCGSNCAPPDAVRAAALP---PQTPPQTRRRRRAKITG-------------- 307
           | | |     |     :  | :  |   |:   : |:    :::
Db     263 ALGGPGFQERGGELKREERTRNSLSPTIAPKLSLEVRKLSNGRLSTSLKLGPLQPRGVPL 322

Qy     308 RERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVNSALNPVI 367
           ||:|| ::: :|:|||::|| |||: |:    |  | | | | || ||||||||||||||
Db     323 REKKATQMVAIVLGAFIVCWLPFFLTHVLNTHCQTCHVSPELYSATTWLGYVNSALNPVI 382

Qy     368 YTVFNAEFRNVFRKAL 383
           || || |||  | | |
Db     383 YTTFNIEFRKAFLKIL 398


RESULT   6
I48322
dopamine receptor D3 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: I48322; S25161
R;Fishburn, C.S.; Belleli, D.; David, C.; Carmon, S.; Fuchs, S.
J. Biol. Chem. 268, 5872-5878, 1993
A;Title: A novel short isoform of the D3 dopamine receptor generated by alternative
A;Reference number: I48322; MUID:93194894
A;Accession: I48322
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-446 <RES>
A;Cross-references: EMBL:X67274; NID:g50651; PIDN:CAA47691.1; PID:g50652
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor


  Query Match             32.9%;  Score 669;  DB 2;  Length 446;
  Best Local Similarity   37.2%;  Pred. No. 6.8e-36;
  Matches  153;  Conservative   54;  Mismatches  128;  Indels   76;  Gaps    8;

Qy      44 LIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLL 103
           || |:: || ||| :|  |||||| ||  :|||| ||||:| ||:|  || || || |
Db      39 LILAIIFGNGLVCAAVLRERALQTTTNYLVVSLAVADLLVATLVMPWVVYLEVTGGVWNF 98

Qy     104 SPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYNR---QGGSRRQLLLIGATW 160
           |   ||  : :|| :||||| ||||||:||: || :|: |     |   ||  |:| | |
Db      99 SRICCDVFVTLDVMMCTASILNLCAISIDRYTAVVMPVHYQHGTGQSSCRRVALMITAVW 158

Qy     161 LLSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQ 220
           :|: ||: |:| | |     ||::| : : |:|:|||| ||::|  : :|:|   :  |:
Db     159 VLAFAVSCPLLFGFNTT--GDPSICSISNPDFVIYSSVVSFYVPFGVTVLVYARIYMVLR 216

Qy     221 RWEVARRAKLHGRAPR-----RPSGPGPPS--------------------------PTP 248
           :   || ::  |        ||  |   |
Db     217 Q---RRRKRILTRQNSQCISIRPGFPQQSSCLRLHPIRQFSIRARFLSDATGQMEHIEDK 273

Qy     249 PAPRLPQDPCGPDCAPPAPGL------------------PPDPCGSNCAPPDAVRAAAL 289
           | |:  |||      | :||                  |    |  :  :  | :
```

```
Db    274 PYPQKCQDPLLSHLQPLSPGQTHGELKRYYSICQDTALRHPNFEGGGGMSQVERTRNSLS 333

Qy    290 PPQTPP---QTRRRRRAKITG-------------RERKAMRVLPVVVGAFLLCWTPFFV 332
          |   |    : |:    :::                ||:|| ::: :|:|||::|| |||:
Db    334 PTMAPKLSLEVRKLSNGRLSTSLKLGPLQPRGVPLREKKATQMVVIVLGAFIVCWLPFFL 393

Qy    333 VHITQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKAL 383
          |:    | || | | |  | ||||||||||||||| || |||  | | |
Db    394 THVLNTHCQACHVSPELYRATTWLGYVNSALNPVIYTTFNIEFRKAFLKIL 444


RESULT   7
D56849
dopamine receptor-like protein D222 - Japanese pufferfish
C;Species: Fugu rubripes (Japanese pufferfish)
C;Date: 27-Oct-1995 #sequence_revision 27-Oct-1995 #text_change 07-May-1999
C;Accession: D56849
R;Macrae, A.D.; Brenner, S.
Genomics 25, 436-446, 1995
A;Title: Analysis of the dopamine receptor family in the compact genome of the puffer fi
A;Reference number: A56849; MUID:95309911
A;Accession: D56849
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-514 <MAC>
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor


  Query Match             32.4%;  Score 658.5;  DB 2;  Length 514;
  Best Local Similarity   34.7%;  Pred. No. 3.6e-35;
  Matches  167;  Conservative   52;  Mismatches  111;  Indels  151;  Gaps   13;

Qy     43 LLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWL 102
          ||| |:: || |||::|  ||:||| ||  :|||| ||||:| ||:|  || || |||||
Db     43 LLILAIVFGNVLVCLAVLRERSLQTTTNYLVVSLAVADLLVASLVMPWAVYLEVVGGAWL 102

Qy    103 LSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQL-LLIGATWL 161
          |   |:  : :|| :||||| ||||||:||: || :|: ||    ||::: ::|   |:
Db    103 FSRLYCNIFVTLDVMMCTASILNLCAISIDRYTAVVMPVLYNTTHRSRKRVFVMIAIVWV 162

Qy    162 LSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQR 221
          |: ||: |:| | |     || || : : |:|:|||| ||:||  : ||:|   :  |:
Db    163 LAFAVSCPLLFGFNTT--DDPMVCSISNPDFVIYSSVVSFYLPFIITLLVYIRIYIFLR- 219

Qy    222 WEVARRAKLHGRAPRRPSGPGPPSPTPPA--------PRLPQD---------------PC 258
              || ::   |  :|||   |   ||:         |:  ||               |
Db    220 ---MRRKRI---AFGQPSGKVQPGSAPPSAETCLQETPQAKQDLSPIRIKVQSVELPGPS 273

Qy    259 GPDCAP-------PAPG------LPPDPCGSNCA-------------------------- 279
          |           |  |       |||    : |:
Db    274 KPSLLSGCLWRKRPKTGPVENSMLPPVDTQNCCSISHASCGRTELDLEQERGEEGEEVAE 333

Qy    280 ------PPDAVRAA-------------ALPP---------------------------- 291
                ||  || :              :| |
Db    334 GSQREQPP--VRMSCEVKDLSNGRTHTSLHPAYHSHTLNTRFRTMHAREKKATQMLAIVL 391

Qy    292 ----QTPP-------------------------QTRRRRRAKITGRERKAMRVLPVVVGA 322
              : ||                         |   |   :  ||:|| ::| :|:|
Db    392 GSQREQPPVRMSCEVKDLSNGRTHTSLHPAYHSHTLNTRFRTMHAREKKATQMLAIVLGV 451

Qy    323 FLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKA 382
          ||:|| |||| ||    |  | :|| | || ||||||||||||||| || |||  | |
Db    452 FLICWLPFFVTHILNTHCRTCYIPPGLYSAFTWLGYVNSALNPVIYTTFNIEFRRAFIKI 511

Qy    383 L 383
          |
Db    512 L 512


RESULT   8
DYHUD2
dopamine receptor D2 - human
```

```
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 21-Jul-2000
C;Accession: S08417; S09618; S20842; A33392; A34502; A37013; A37384; A48409; S40694
R;Robakis, N.K.; Mohamadi, M.; Fu, D.Y.; Sambamurti, K.; Refolo, L.M.
Nucleic Acids Res. 18, 1299, 1990
A;Title: Human retina D2 receptor cDNAs have multiple polyadenylation sites and diff
A;Reference number: S08417; MUID:90206805
A;Accession: S08417
A;Molecule type: mRNA
A;Residues: 1-443 <ROB>
A;Cross-references: EMBL:X51362; NID:g30495; PIDN:CAA35746.1; PID:g30496
R;dal Toso, R.; Sommer, B.; Ewert, M.; Herb, A.; Pritchett, D.B.; Bach, A.; Shivers,
EMBO J. 8, 4025-4034, 1989
A;Title: The dopamine D2 receptor: two molecular forms generated by alternative spli
A;Reference number: S09618; MUID:90076122
A;Accession: S09618
A;Molecule type: mRNA
A;Residues: 1-443 <DAL>
A;Cross-references: EMBL:X51645; NID:g30867; PIDN:CAB56463.1; PID:g5921480
A;Accession: S20842
A;Molecule type: DNA
A;Residues: 179-379 <DA2>
A;Cross-references: EMBL:X51646; NID:g30868; PIDN:CAB37869.1; PID:g4467834
R;Selbie, L.A.; Hayes, G.; Shine, J.
DNA 8, 683-689, 1989
A;Title: The major dopamine D2 receptor: molecular analysis of the human D2-A subtyp
A;Reference number: A33392; MUID:90126238
A;Accession: A33392
A;Molecule type: mRNA
A;Residues: 1-443 <SEL>
A;Cross-references: GB:M30625; NID:g181431; PIDN:AAA88024.1; PID:g181432
R;Grandy, D.K.; Marchionni, M.A.; Makam, H.; Stofko, R.E.; Alfano, M.; Frothingham,
Proc. Natl. Acad. Sci. U.S.A. 86, 9762-9766, 1989
A;Title: Cloning of the cDNA and gene for a human D-2 dopamine receptor.
A;Reference number: A34502; MUID:90099344
A;Accession: A34502
A;Molecule type: mRNA
A;Residues: 1-443 <GRA>
A;Cross-references: GB:M29066; NID:g181828; PIDN:AAA52761.1; PID:g181829; GB:M77247;
R;Stormann, T.M.; Gdula, D.C.; Weiner, D.M.; Brann, M.R.
Mol. Pharmacol. 37, 1-6, 1990
A;Title: Molecular cloning and expression of a dopamine D2 receptor from human retin
A;Reference number: A37013; MUID:90136534
A;Accession: A37013
A;Molecule type: mRNA
A;Residues: 1-241,271-443 <STO>
R;Selbie, L.A.; Hayes, G.; Shine, J.
Adv. Second Messenger Phosphoprotein Res. 24, 9-14, 1990
A;Title: DNA homology screening: isolation and characterization of the human D2-A do
A;Reference number: A37384; MUID:91000955
A;Accession: A37384
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-443 <SE2>
A;Experimental source: fetal brain and pituitary
R;Dearry, A.; Falardeau, P.; Shores, C.; Caron, M.G.
Cell. Mol. Neurobiol. 11, 437-453, 1991
A;Title: D2 dopamine receptors in the human retina: cloning of cDNA and localization
A;Reference number: A48409; MUID:92076439
A;Accession: A48409
A;Molecule type: mRNA
A;Residues: 1-241,271-443 <DEA>
A;Cross-references: GB:S69899; NID:g240290; PIDN:AAB20571.1; PID:g240291
A;Experimental source: retina
A;Note: sequence extracted from NCBI backbone (NCBIN:69899, NCBIP:69900)
R;Araki, K.; Kuwano, R.; Morii, K.; Hayashi, S.; Minoshima, S.; Shimizu, N.; Katagir
Neurochem. Int. 21, 91-98, 1992
A;Title: Structure and expression of human and rat D2 dopamine receptor genes.
A;Reference number: S40694; MUID:93264902
A;Accession: S40694
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-39,'R',41-443 <ARA>
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A;Cross-references: GB:S62137; NID:g405309; PIDN:AAB26819.1; PID:g405310
C;Genetics:
A;Gene: GDB:DRD2
A;Cross-references: GDB:119852; OMIM:126450
A;Map position: 11q23.1-11q23.1
A;Introns: 178/1; 241/3; 270/3; 380/1
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; lipoprotein;
F;1-443/Product: dopamine receptor D2 (long form) #status predicted <MAT1>
F;1-241,271-443/Product: dopamine receptor D2 (short form) #status predicted <MAT2>
F;38-59/Domain: transmembrane #status predicted <TM1>
F;71-94/Domain: transmembrane #status predicted <TM2>
F;109-130/Domain: transmembrane #status predicted <TM3>
F;152-174/Domain: transmembrane #status predicted <TM4>
F;188-210/Domain: transmembrane #status predicted <TM5>
F;211-373/Domain: intracellular #status predicted <CYT>
F;374-397/Domain: transmembrane #status predicted <TM6>
F;406-429/Domain: transmembrane #status predicted <TM7>
F;5,17,23/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;107-182/Disulfide bonds: #status predicted
F;443/Binding site: palmitate (Cys) (covalent) #status predicted


  Query Match             31.8%;  Score 645;  DB 1;  Length 443;
  Best Local Similarity   39.1%;  Pred. No. 2.3e-34;
  Matches  160;  Conservative   51;  Mismatches  120;  Indels   78;  Gaps   14;

Qy      43 LLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWL 102
           |||  :: || |||::|: |:|||| ||  ||||| ||||:| ||:|  || ||  | |
Db      43 LLIAVIVFGNVLVCMAVSREKALQTTTNYLIVSLAVADLLVATLVMPWVVYLEVV-GEWK 101

Qy     103 LSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYN-RQGGSRRQLLLIGATWL 161
           |   ||  : :|| :|||| |||||:|: |||:|: || |    ||  ::|   |:
Db     102 FSRIHCDIFVTLDVMMCTASILNLCAISIDRYTAVAMPMLYNTRYSSKRRVTVMISIVWV 161

Qy     162 LSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQR 221
           ||  :: |:| |||:    |   | : :  :|||||: ||::|  : ||:|   :  |:|
Db     162 LSFTISCPLLFGLNNA---DQNECIIANPAFVVYSSIVSFYVPFIVTLLVYIKIYIVLRR 218

Qy     222 -------WEVARRAKLHGRAP----------------------------------RRP-- 238
                  :|  : | |||                                     ||
Db     219 RRKRVNTKRSSRAFRAHLRAPLKGNCTHPEDMKLCTVIMKSNGSFPVNRRRVEAARRAQE 278

Qy     239 ------SGPGPP-----SPTPPAPR---LPQDPC--GPDCAPPAPGLPPDPCGSNCAPPD 282
                |   ||     || ||:     || ||   |    | :|  |       |    |
Db     279 LEMEMLSSTSPPERTRYSPIPPSHHQLTLP-DPSHHGLHSTPDSPAKPE----KNGHAKD 333

Qy     283 AVRAAAL-PPQTPPQTRRRRRAKITGR-------ERKAMRVLPVVVGAFLLCWTPFFVVH 334
             : | :   || |  : |   |   |        |:|| ::| :|:| |::|| |||: |
Db     334 HPKIAKIFEIQTMPNGKTRTSLKTMSRRKLSQQKEKKATQMLAIVLGVFIICWLPFFITH 393

Qy     335 ITQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKAL 383
           |    |  |::|| | || |||||||||:||:||| || |||  | | |
Db     394 ILNIHCD-CNIPPVLYSAFTWLGYVNSAVNPIIYTTFNIEFRKAFLKIL 441


RESULT   9
C56849
dopamine receptor-like protein D215 - Japanese pufferfish
C;Species: Fugu rubripes (Japanese pufferfish)
C;Date: 27-Oct-1995 #sequence_revision 27-Oct-1995 #text_change 07-May-1999
C;Accession: C56849
R;Macrae, A.D.; Brenner, S.
Genomics 25, 436-446, 1995
A;Title: Analysis of the dopamine receptor family in the compact genome of the puffer fi
A;Reference number: A56849; MUID:95309911
A;Accession: C56849
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-511 <MAC>
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor


 Query Match             31.4%;  Score 638;  DB 2;  Length 511;
 Best Local Similarity   32.6%;  Pred. No. 7.3e-34;
 Matches  155;  Conservative   62;  Mismatches  118;  Indels  140;  Gaps   10;

Qy      43 LLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWL 102
           |||  :: || |||::|: |:|||| ||  ||||| ||||:| ||:|  || ||  | |
Db      41 LLIFVIVFGNVLVCMAVSREKALQTTTNYLIVSLAVADLLVATLVMPWVVYLEVV-GEWR 99

Qy     103 LSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQL-LLIGATWL 161
           |   ||  : :|| :|||| ||||||:||: |||:|: || :  |||:: ::|   |:
Db     100 FSKIHCDIFVTLDVMMCTASILNLCAISIDRYTAVAMPMLYNTRYSSRRRVTVMISVVWV 159

Qy     162 LSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQR 221
           || |:: |:| |||:   || ::| : :  :|||||: ||::|  : ||:|   :  |::
Db     160 LSFAISCPLLFGLNNTATRDQSLCFIANPAFVVYSSIVSFYVPFIVTLLVYVQIYVVLRK 219

Qy     222 WEVARRAKLHGRAPRR-PSGPGPPSPT------------------------------- 247
               || ::: :  :|      |  ||
Db     220 ----RRKRVNTKPKQRLCQAADPDIPTSLKDKCTHPEDVRLCTMIVKSNGSFPVNKKKVI 275

Qy     248 --------------------------PPAPRLP----------------QDPCGPDCAP 264
                                       ||  : |                :    |  |
Db     276 FIKDGVNEVEGLELDELNYCGGSHKQPPPQQQPRALGDTPATSHQLLMSTKANASPTSTP 335

Qy     265 PAP----------GLPPDPCGSNCAPPDAVR--------------------------A 286
           | |          | |     | ||  |:|                          |
Db     336 PTPPEEGQRTEKNGDPTKEAQGNPAPVVALRNGKTQTSLKTLSKRKISQQKEKKATQMLA 395

Qy     287 AALP-----------------PQTPPQTRRRRRAKITGRERKAMRVLPVVVGAFLLCWT 328
             ||                 ||  :|  :|:     :|:|| ::| :|:| |::||
Db     396 IVLPTKEAQGNPAPVVALRNGKTQTSLKTLSKRKIS-QQKEKKATQMLAIVLGVFIICWL 454

Qy     329 PFFVVHITQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKAL 383
           |||: ||    |  | ||  : :| |||||||||:||:||| || |||  | | |
Db     455 PFFITHILNTHCTRCKVPAEMYNAFTWLGYVNSAVNPIIYTTFNVEFRKAFIKIL 509


RESULT  10
DYBOD2
dopamine receptor D2 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C;Accession: S08163
R;Chio, C.L.; Hess, G.F.; Graham, R.S.; Huff, R.M.
Nature 343, 266-269, 1990
A;Title: A second molecular form of D2 dopamine receptor in rat and bovine caudate nu
A;Reference number: S08163; MUID:90136899
A;Accession: S08163
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-444 <CHI>
A;Cross-references: GB:X51657; NID:g304; PIDN:CAA35970.1; PID:g305
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; lipoprotc
F;1-444/Product: dopamine receptor D2 (long form) #status predicted <MAT1>
F;1-241,271-444/Product: dopamine receptor D2 (short form) #status predicted <MAT2>
F;39-59/Domain: transmembrane #status predicted <TM1>
F;71-94/Domain: transmembrane #status predicted <TM2>
F;109-130/Domain: transmembrane #status predicted <TM3>
F;152-174/Domain: transmembrane #status predicted <TM4>
F;188-210/Domain: transmembrane #status predicted <TM5>
F;211-374/Domain: intracellular #status predicted <CYT>
F;375-398/Domain: transmembrane #status predicted <TM6>
F;407-430/Domain: transmembrane #status predicted <TM7>
F;5,17,23/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;107-182/Disulfide bonds: #status predicted
F;444/Binding site: palmitate (Cys) (covalent) #status predicted


  Query Match             31.3%;  Score 636.5;  DB 1;  Length 444;
  Best Local Similarity   38.2%;  Pred. No. 8e-34;
  Matches  156;  Conservative   53;  Mismatches  124;  Indels   75;  Gaps   13;
```

```
Qy      43 LLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWL 102
           |||  :: || |||::|: |:|||| ||  ||||| ||||:| ||:|  || ||  | |
Db      43 LLIFVIVFGNVLVCMAVSREKALQTTTNYLIVSLAVADLLVATLVMPWVVYLEVV-GEWK 101

Qy     103 LSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYN-RQGGSRRQLLLIGATWL 161
           |   ||  : :|| :|||| ||||||:||: |||:|: || |    ||  ::|   |:
Db     102 FSRIHCDIFVTLDVMMCTASILNLCAISIDRYTAVAMPMLYNTRYSSKRRVTVMIAIVWV 161

Qy     162 LSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQR 221
           ||  :: |:| |||:    |   | : :  :|||||: ||::|  : ||:|   :  |:|
Db     162 LSFTISCPMLFGLNNT---DQNECIIANPAFVVYSSIVSFYVPFIVTLLVYIKIYIVLRR 218

Qy     222 ------------WEVARRAKLHG---------------------------RAPRRP-- 238
                       :   :| | |                           | ||
Db     219 RRKRVNTKRSSRAFRANLKAPLKGNCTHPEDMKLCTVIMKSNGSFPVNRRRVEAARRAQE 278

Qy     239 ------SGPGPP-----SPTPPAPR---LPQDPC--GPDCAPPAPGLPPDPCGSNCAPPD 282
                |   ||     || ||:     || ||   |    | :|  |     :    |
Db     279 LEMEMLSSTSPPERTRYSPIPPSHHQLTLP-DPSHHGLHSTPDSPAKPEKNGHAKTVNPK 337

Qy     283 AVRAAALPPQTPPQTRRRRRAKITGR-------ERKAMRVLPVVVGAFLLCWTPFFVVHI 335
             :   :  |: |  : |   |   |       |:|| ::| :|:| |::|| |||: ||
Db     338 IAKIFEI--QSMPNGKTRTSLKTMSRRKLSQQKEKKATQMLAIVLGVFIICWLPFFITHI 395

Qy     336 TQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKAL 383
              |  |::|| | || ||||||||:||:||| || |||  | | |
Db     396 LNIHCD-CNIPPVLYSAFTWLGYVNSAVNPIIYTTFNIEFRKAFLKIL 442
```

RESULT 11
DYMSD2
dopamine receptor D2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C;Accession: S13921; JH0452; JH0453
R;Montmayeur, J.P.; Bausero, P.; Amlaiky, N.; Maroteaux, L.; Hen, R.; Borrelli, E.
FEBS Lett. 278, 239-243, 1991
A;Title: Differential expression of the mouse D(2) dopamine receptor isoforms.
A;Reference number: S13921; MUID:91122293
A;Accession: S13921
A;Molecule type: mRNA
A;Residues: 1-444 <MON>
A;Cross-references: EMBL:X55674; NID:g50648; PIDN:CAA39209.1; PID:g50649
R;Mack, K.J.; Todd, R.D.; O'Malley, K.L.
J. Neurochem. 57, 795-801, 1991
A;Title: The mouse dopamine D2A receptor gene: sequence homology with the rat and human
A;Reference number: JH0452; MUID:91318281
A;Accession: JH0452
A;Molecule type: DNA
A;Residues: 1-24,'C',26-28,'P',30-88,'R',90-103,'S',105-270,'P',252-444 <MAC>
A;Note: the authors translated the codon CAG for residue 16 as Glu
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; lipoprotein;
F;1-444/Product: dopamine receptor D2 (long form) #status predicted <MAT1>
F;1-241,271-444/Product: dopamine receptor D2 (short form) #status predicted <MAT2>
F;38-59/Domain: transmembrane #status predicted <TM1>
F;71-94/Domain: transmembrane #status predicted <TM2>
F;109-130/Domain: transmembrane #status predicted <TM3>
F;152-174/Domain: transmembrane #status predicted <TM4>
F;188-210/Domain: transmembrane #status predicted <TM5>
F;211-374/Domain: intracellular #status predicted <CYT>
F;375-398/Domain: transmembrane #status predicted <TM6>
F;407-430/Domain: transmembrane #status predicted <TM7>
F;5,17,23/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;107-182/Disulfide bonds: #status predicted
F;147,148,228,229,355,360,365/Binding site: phosphate (Ser) (covalent) #status predicted
F;225,373/Binding site: phosphate (Thr) (covalent) #status predicted
F;444/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 31.1%; Score 631.5; DB 1; Length 444;
Best Local Similarity 38.2%; Pred. No. 1.7e-33;

Matches 156; Conservative 51; Mismatches 126; Indels 75; Gaps 13;

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Qy      43 LLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWL 102
           |||  :: || |||::|: |:|||| ||  ||||| ||||:| ||:|  || ||  | |
Db      43 LLIFIIVFGNVLVCMAVSREKALQTTTNYLIVSLAVADLLVATLVMPWVVYLEVV-GEWK 101

Qy     103 LSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYN-RQGGSRRQLLLIGATWL 161
           |   ||  : :|| :|||| ||||||:||: |||:|: || |    ||  ::|   |:
Db     102 FSRIHCDIFVTLDVMMCTASILNLCAISIDRYTAVAMPMLYNTRYSSKRRVTVMIAIVWV 161

Qy     162 LSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWA------- 214
           ||  :: |:| |||:    |   | : :  :|||||: ||::|  : ||:|
Db     162 LSFTISCPLLFGLNNT---DQNECIIANPAFVVYSSIVSFYVPFIVTLLVYIKIYIVLRK 218

Qy     215 ------TFRGLQRWEVARRAKLHGR---------------------------APRRP-- 238
                 | |  : :    :  | |                           | ||
Db     219 RRKRVNTKRSSRAFRANLKTPLKGNCTHPEDMKLCTVIMKSNGSFPVNRRRMDAARRAQE 278

Qy     239 ------SGPGPP-----SPTPPAPR---LPQDPC--GPDCAPPAPGLPPDPCGSNCAPPD 282
                |   ||     || ||:     || ||   |    | :|  |     :    |
Db     279 LEMEMLSSTSPPERTRYSPIPPSHHQLTLP-DPSHHGLHSNPDSPAKPEKNGHAKIVNPR 337

Qy     283 AVRAAALPPQTPPQTRRRRRAKITGR-------ERKAMRVLPVVVGAFLLCWTPFFVVHI 335
             :   :  || |  : |   |   |       |:|| ::| :|:| |::|| |||: ||
Db     338 IAKFFEI--QTMPNGKTRTSLKTMSRRKLSQQKEKKATQMLAIVLGVFIICWLPFFITHI 395

Qy     336 TQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKAL 383
              |  |::|| | || ||||||||:||:||| || |||  | | |
Db     396 LNIHCD-CNIPPVLYSAFTWLGYVNSAVNPIIYTTFNIEFRKAFMKIL 442
```

RESULT 12
S08146
dopamine receptor D2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C;Accession: S08146; S19610; S07791; S09040; S09097; S19251; S08145; A34046; S21548;
R;Monsma Jr., F.J.; McVittie, L.D.; Gerfen, C.R.; Mahan, L.C.; Sibley, D.R.
Nature 342, 926-929, 1989
A;Title: Multiple D2 dopamine receptors produced by alternative RNA splicing.
A;Reference number: S08146; MUID:90081873
A;Accession: S08146
A;Molecule type: mRNA
A;Residues: 1-444 <MON>
A;Cross-references: EMBL:X17458
R;Chio, C.L.; Hess, G.F.; Graham, R.S.; Huff, R.M.
Nature 343, 266-269, 1990
A;Title: A second molecular form of D2 dopamine receptor in rat and bovine caudate nu
A;Reference number: S08163; MUID:90136899
A;Accession: S19610
A;Molecule type: mRNA
A;Residues: 1-444 <CHI>
R;Bunzow, J.R.; van Tol, H.H.M.; Grandy, D.K.; Albert, P.; Salon, J.; Christie, M.; K
Nature 336, 783-787, 1988
A;Title: Cloning and expression of a rat D(2) dopamine receptor cDNA.
A;Reference number: S07791; MUID:89082643
A;Accession: S07791
A;Molecule type: mRNA
A;Residues: 1-241,271-444 <BUN>
A;Cross-references: EMBL:X14028
R;Rao, D.D.; McKelvy, J.; Kebabian, J.; MacKenzie, R.G.
FEBS Lett. 263, 18-22, 1990
A;Title: Two forms of the rat D(2) dopamine receptor as revealed by the polymerase ch
A;Reference number: S09040; MUID:90235966
A;Accession: S09040
A;Molecule type: mRNA
A;Residues: 1-98,'D',100-172,'R',174-179,'G',181-444 <RAO>
A;Cross-references: GB:X53278; NID:g288117; PIDN:CAA37373.1; PID:g288118
R;O'Dowd, B.F.; Nguyen, T.; Tirpak, A.; Jarvie, K.R.; Israel, Y.; Seeman, P.; Niznik,
FEBS Lett. 262, 8-12, 1990
A;Title: Cloning of two additional catecholamine receptors from rat brain.
A;Reference number: S09096; MUID:90201380
A;Accession: S09097

A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 126-303 <ODO>
R;dal Toso, R.; Sommer, B.; Ewert, M.; Herb, A.; Pritchett, D.B.; Bach, A.; Shivers, B.D
EMBO J. 8, 4025-4034, 1989
A;Title: The dopamine D2 receptor: two molecular forms generated by alternative splicing
A;Reference number: S09618; MUID:90076122
A;Accession: S19251
A;Molecule type: mRNA
A;Residues: 175-299 <DAL>
R;Giros, B.; Sokoloff, P.; Martres, M.P.; Riou, J.F.; Emorine, L.J.; Schwartz, J.C.
Nature 342, 923-926, 1989
A;Title: Alternative splicing directs the expression of two D2 dopamine receptor isoform
A;Reference number: S08145; MUID:90081872
A;Accession: S08145
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 239-272 <GIR>
R;Miller, J.C.; Wang, Y.; Filer, D.
Biochem. Biophys. Res. Commun. 166, 109-112, 1990
A;Title: Identification by sequence analysis of a second rat brain cDNA encoding the dop
A;Reference number: A34046; MUID:90147685
A;Accession: A34046
A;Molecule type: mRNA
A;Residues: 242-270 <MIL>
A;Cross-references: GB:M32241; NID:g203902; PIDN:AAA41074.1; PID:g203904
R;Taylor, P.L.; Inglis, J.D.; Eidne, K.A.
submitted to the EMBL Data Library, October 1990
A;Description: 5' untranslated region of rat pituitary dopamine D2(B) receptor contains
A;Reference number: S21548
A;Accession: S21548
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-444 <TAY>
A;Cross-references: EMBL:X56065; NID:g56063; PIDN:CAA39543.1; PID:g56064
C;Genetics:
A;Introns: 241/3; 270/3; 381/1
A;Note: the list of introns may be incomplete
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; lipoprotein;
F;1-444/Product: dopamine receptor D2 (long form) #status predicted <MAT1>
F;1-241,271-444/Product: dopamine receptor D2 (short form) #status predicted <MAT2>
F;38-59/Domain: transmembrane #status predicted <TM1>
F;71-94/Domain: transmembrane #status predicted <TM2>
F;109-130/Domain: transmembrane #status predicted <TM3>
F;152-174/Domain: transmembrane #status predicted <TM4>
F;188-210/Domain: transmembrane #status predicted <TM5>
F;211-374/Domain: intracellular #status predicted <INT>
F;375-398/Domain: transmembrane #status predicted <TM6>
F;407-430/Domain: transmembrane #status predicted <TM7>
F;5,17,23/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;107-182/Disulfide bonds: #status predicted
F;228,229/Binding site: phosphate (Ser) (covalent) #status predicted
F;444/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 31.1%; Score 631.5; DB 1; Length 444;
Best Local Similarity 38.2%; Pred. No. 1.7e-33;
Matches 156; Conservative 51; Mismatches 126; Indels 75; Gaps 13;

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Qy      43 LLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWL 102
           |||  :: || |||::|: |:|||| ||  ||||| ||||:| ||:|  || ||  | |
Db      43 LLIFIIVFGNVLVCMAVSREKALQTTTNYLIVSLAVADLLVATLVMPWVVYLEVV-GEWK 101

Qy     103 LSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYN-RQGGSRRQLLLIGATWL 161
           |   ||  : :|| :|||||| ||||||:||: |||:|: || |    ||  ::|   |:
Db     102 FSRIHCDIFVTLDVMMCTASILNLCAISIDRYTAVAMPMLYNTRYSSKRRVTVMIAIVWV 161

Qy     162 LSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWA------- 214
           ||  :: |:| |||:    |   | : :  :|||||: ||::|  : ||:|
Db     162 LSFTISCPLLFGLNNT---DQNECIIANPAFVVYSSIVSFYVPFIVTLLVYIKIYIVLRK 218

Qy     215 ------TFRGLQRWEVARRAKLHGR---------------------------APRRP-- 238
```

```
                |  |  : :    :  | |                                  | ||
Db     219 RRKRVNTKRSSRAFRANLKTPLKGNCTHPEDMKLCTVIMKSNGSFPVNRRRMDAARRAQE 278

Qy     239 ------SGPGPP-----SPTPPAPR---LPQDPC--GPDCAPPAPGLPPDPCGSNCAPPD 282
                |   ||     || ||:     || ||   |    | :|  |     :    |
Db     279 LEMEMLSSTSPPERTRYSPIPPSHHQLTLP-DPSHHGLHSNPDSPAKPEKNGHAKIVNPR 337

Qy     283 AVRAAALPPQTPPQTRRRRRAKITGR-------ERKAMRVLPVVVGAFLLCWTPFFVVHI 335
             :   :  || |  : |   |   |       |:|| ::| :|:|  |::|| |||: ||
Db     338 IAKFFEI--QTMPNGKTRTSLKTMSRRKLSQQKEKKATQMLAIVLGVFIICWLPFFITHI 395

Qy     336 TQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKAL 383
             |  |::|| | || |||||||||:||:||| || |||. | | |
Db     396 LNIHCD-CNIPPVLYSAFTWLGYVNSAVNPIIYTTFNIEFRKAFMKIL 442
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RESULT 13
DYXLD2
dopamine receptor D2 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
C;Accession: S14827
R;Martens, G.J.M.; Molhuizen, H.O.F.; Groeneveld, D.; Roubos, E.W.
FEBS Lett. 281, 85-89, 1991
A;Title: Cloning and sequence analysis of brain cDNA encoding a Xenopus D(2) dopamine
A;Reference number: S14827; MUID:91200321
A;Accession: S14827
A;Molecule type: mRNA
A;Residues: 1-442 <MAR>
A;Cross-references: EMBL:X59500; NID:g64648; PIDN:CAA42088.1; PID:g64649
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; neurotran
F;1-442/Product: dopamine receptor D2 (long form) #status predicted <MAT1>
F;1-232,266-442/Product: dopamine receptor D2 (short form) #status predicted <MAT2>
F;32-53/Domain: transmembrane #status predicted <TM1>
F;65-88/Domain: transmembrane #status predicted <TM2>
F;103-124/Domain: transmembrane #status predicted <TM3>
F;146-168/Domain: transmembrane #status predicted <TM4>
F;182-204/Domain: transmembrane #status predicted <TM5>
F;205-372/Domain: intracellular #status predicted <INT>
F;373-396/Domain: transmembrane #status predicted <TM6>
F;405-428/Domain: transmembrane #status predicted <TM7>
F;5,15,18,169/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;223/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 31.0%; Score 629.5; DB 1; Length 442;
Best Local Similarity 36.4%; Pred. No. 2.2e-33;
Matches 151; Conservative 59; Mismatches 120; Indels 85; Gaps 12;

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Qy      43 LLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWL 102
           ||:  :: || |||::|: |:|||| ||  ||||| ||||:| ||:|  || ||  | |
Db      37 LLVFVIVFGNVLVCIAVSREKALQTTTNYLIVSLAVADLLVATLVMPWAVYMEVV-GEWR 95

Qy     103 LSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYN-RQGGSRRQLLLIGATWL 161
           |   ||  : :|| :|||||| ||||||:||: |||:|: || |    ||  ::|   |:
Db      96 FSRIHCDIFVTLDVMMCTASILNLCAISIDRYTAVAMPMLYNTRYSSKRRVTVMISVVWV 155

Qy     162 LSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQR 221
           || |:: |:| |||:    :   || :::  :|:|||: ||::|  : ||:|      :|
Db     156 LSFAISCPLLFGLNNTGSK---VCIIDNPAFVIYSSIVSFYVPFIVTLLVY------VQI 206

Qy     222 WEVARR-----------------------------------AKLHGRAPR--------RP 238
           : | |:                                    | :|  |         :
Db     207 YIVLRKRRKRVNTKRNSRGVAVDAHKDKCTHPEDVKLCSVFVKSNGSFPADKKKVILVQE 266

Qy     239 SGPGPP-------SPTPPAPRLPQDPCGPD---CAPPA------------PGLPPDPCGS 276
           :|  |        | | |  :      ||     | ||              |   |
Db     267 AGKHPEDMEMEMMSSTSPPEKTKHKSASPDHNQLAVPATSNQCKNASLTSPVESPYKAEK 326

Qy     277 NCAPPDAVR-AAALPPQTPPQTRRRRRAKITG-------RERKAMRVLPVVVGAFLLCWT 328
           |  | |: : |      |: |  : |   |          :|:|| ::| :|:| |::||
Db     327 NGHPKDSTKPAKVFEIQSMPNGKTRTSIKTMSKKKLSQHKEKKATQMLAIVLGVFIICWL 386
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Qy     329 PFFVVHITQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKAL 383
           |||::||    |  |.::|  | || |||||||||:||:||| || |||  | | |
Db     387 PFFIIHILNMHC-NCNIPQALYSAFTWLGYVNSAVNPIIYTTFNVEFRKAFIKIL 440


RESULT  14
A38316
alpha-2-adrenergic receptor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
C;Accession: A38316
R;Guyer, C.A.; Horstman, D.A.; Wilson, A.L.; Clark, J.D.; Cragoe Jr., E.J.; Limbird, L.E
J. Biol. Chem. 265, 17307-17317, 1990
A;Title: Cloning, sequencing, and expression of the gene encoding the porcine alpha-2-ad
A;Reference number: A38316; MUID:91009167
A;Accession: A38316
A;Molecule type: DNA
A;Residues: 1-450 <GUY>
A;Cross-references: GB:J05652; NID:g164303; PIDN:AAA30984.1; PID:g164304
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein


  Query Match             28.6%;  Score 581;  DB 2;  Length 450;
  Best Local Similarity   34.1%;  Pred. No. 2.9e-30;
  Matches  152;  Conservative   62;  Mismatches  142;  Indels   90;  Gaps   13;

Qy      18 PAAGASAGASAGLAGQGAAA------------LVGGVLLIGAVLAGNSLVCVSVATERAL 65
           | || ::       | || |             : |:|::  |  || || ::| | |||
Db       6 PEAGNASWNGTEAPGGGARATPYSLQVTLTLVCLAGLLMLFTVF-GNVLVIIAVFTSRAL 64

Qy      66 QTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCTASIFN 125
           : | | |:||||:||:|:| ||:|  : :||  | |      |:  :|:|:|  ||:|| :
Db      65 KAPQNLFLVSLASADILVATLVIPFSLANEVM-GYWYFGKAWCEIYLALDVLFCTSSIVH 123

Qy     126 LCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVR---GRDP 182
           ||||||:||: ::   : || :   ||   :|   |::|| :: | |  :       |: |
Db     124 LCAISLDRYWSITQAIEYNLKRTPRRIKAIIVTVWVISAVISFPPLISIEKKAGGGGQQP 183

Qy     183 AVCRLEDRD---YVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARR---------- 227
           |  | |  |   ||: | : ||| || :|:|:|      :: :::|:|
Db     184 AEPRCEINDQKWYVISSCIGSFFAPCLIMILVY------VRIYQIAKRRTRVPPSRRGPD 237

Qy     228 --AKLHGRAPRRPSGPGPP------------------SPTPPAPRLPQDPCGPDCAPPA 266
             | | | | |||:| ||                   :|  |||  |:|  | |   :
Db     238 AAAALPGGAERRPNGLGPERGVGRVGAEAEPLPVQLNGAPGEPAPAGPRDADGLDLEESS 297

Qy     267 PG----LPPDPCGSNCAPPDAVRAAA--------LP-----------PQTPPQTRRRRA 303
           ||  |  .  |    :| |         ||           | |     |   |
Db     298 SSEHAERPPGPRRSERGPRAKSKARASQVKPGDSLPRRGPGAPGPGAPATGAGEERGGVA 357

Qy     304 KIT------GRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLG 357
           | :       ||::   || ||:| |::|| |||  :   |:  ||||| |     | |
Db     358 KASRWRGRQNREKRFTFVLAVVIGVFVVCWFPFFFTYTLTAV--GCSVPPTLFKFFFWFG 415

Qy     358 YVNSALNPVIYTVFNAEFRNVFRKAL 383
           | ||:|||||||:|| :||  |:| |
Db     416 YCNSSLNPVIYTIFNHDFRRAFKKIL 441


RESULT  15
A37223
alpha-2B-adrenergic receptor - human
N;Alternate names: alpha-2C2-adrenergic receptor
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 29-Oct-1999
C;Accession: A37223; I39407; S14308; A36158
R;Weinshank, R.L.; Zgombick, J.M.; Macchi, M.; Adham, N.; Lichtblau, H.; Branchek, T.A.;
Mol. Pharmacol. 38, 681-688, 1990
A;Title: Cloning, expression, and pharmacological characterization of a human alpha-2B-a
A;Reference number: A37223; MUID:91042469
A;Accession: A37223
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-450 <WEI>
R;Lomasney, J.W.; Lorenz, W.; Allen, L.F.; King, K.; Regan, J.W.; Yang-Feng, T.L.; C
Proc. Natl. Acad. Sci. U.S.A. 87, 5094-5098, 1990
A;Title: Expansion of the alpha 2-adrenergic receptor family: cloning and characteri
A;Reference number: I39407; MUID:90311349
A;Accession: I39407
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-450 <LOM>.
A;Cross-references: GB:M34041; NID:g178197; PIDN:AAA51666.1; PID:g178198
R;Chhajlani, V.; Rangel, N.; Uhlen, S.; Wikberg, J.E.S.
FEBS Lett. 280, 241-244, 1991
A;Title: Identification of an additional gene belonging to the alpha(2) adrenergic re
A;Reference number: S14308; MUID:91192139
A;Accession: S14308
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 56-185 <CHH>
A;Cross-references: GB:X59684; NID:g28635
A;Note: this translation is not annotated in GenBank entry HSALPH218, release 111.0
R;Chang, A.C.; Ho, T.F.; Chang, N.C.
Biochem. Biophys. Res. Commun. 172, 817-823, 1990
A;Title: In vitro amplification by polymerase chain reaction of a partial gene encodi
A;Reference number: A36158; MUID:91054503
A;Accession: A36158
A;Molecule type: DNA
A;Residues: 95-361,'QL',364-389 <CHA>
A;Cross-references: GB:M38742; NID:g177867; PIDN:AAA62823.1; PID:g177868
C;Genetics:
A;Gene: GDB:ADRA2B; ADRARL1; ADRA2L1; ADRA2RL1
A;Cross-references: GDB:120539; OMIM:104260
A;Map position: 2p13-2q13
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein


  Query Match             28.3%;  Score 574.5;  DB 2;  Length 450;
  Best Local Similarity   33.3%;  Pred. No. 7.5e-30;
  Matches  148;  Conservative   65;  Mismatches  126;  Indels  105;  Gaps   15;

Qy      33 QGAAALVGGV-LLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLF 91
           |  ||:   :  ||   : ||:|| ::| | |:|: | | |:|||||||:|:| |::|
Db      10 QATAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADILVATLIIPFS 69

Qy      92 VYSEVQGGAWLLSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYNRQGGSRR 151
           : :|:  | |      |:  :|:||  ||:|| :|||||:||: ||:  | || :   ||
Db      70 LANELL-GYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPRR 128

Qy     152 QLLLIGATWLLSAAVAAPVLCGLND----VRGRDPAVCRL-EDRDYVVYSSVCSFFLPCP 206
              :|   ||::| :: | |    |     |||   |:| ::  |:: ||: ||| ||
Db     129 IKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQ--CKLNQEAWYILASSIGSFFAPCL 186

Qy     207 LMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSGPGPPSPTPPAP---------RLP--- 254
           :|:|:|      |: : :|:|:  : | ||   |||      | |         :||
Db     187 IMILVY------LRIYLIAKRS--NRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALA 238

Qy     255 ----------------------QDPCGPDCAPPAPGLPPDP--------CGSN------ 277
                                  :  |    ||:    |:          ||::
Db     239 SVASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAE 298

Qy     278 -----------CAP---PDAVRAAALPPQTPPQTRR----------------------R 300
                     | |   | :  :|  ||   ||  |                       |
Db     299 EEEEEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWR 358

Qy     301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPA-CSVPPRLVSAVTWLGYV 359
           ||| :| ||::   || ||:| |:||| |||  :   |:||  | ||  |     |:||
Db     359 RRAHVT-REKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPKHCKVPHGLFQFFFWIGYC 417

Qy     360 NSALNPVIYTVFNAEFRNVFRKAL 383
           ||:|||||||:|| :||  ||: |
Db     418 NSSLNPVIYTIFNQDFRRAFRRIL 441
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Search completed: February 13, 2002, 17:39:35
Job time: 121 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: February 13, 2002, 17:39:14 ; Search time 13.31 Seconds
(without alignments)
1066.062 Million cell updates/sec

Title: US-09-550-103-1
Perfect score: 2031
Sequence: 1 MGNRSTADADGLLAGRGPAA.....YTVFNAEFRNVFRKALRACC 387

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1976	97.3	467	1	D4DR_HUMAN	P21917 homo sapien
2	1510	74.3	387	1	D4DR_MOUSE	P51436 mus musculu
3	1496	73.7	387	1	D4DR_RAT	P30729 rattus norv
4	683	33.6	446	1	D3DR_RAT	P19020 rattus norv
5	679	33.4	400	1	D3DR_HUMAN	P35462 homo sapien
6	675	33.2	400	1	D3DR_CERAE	P52703 cercopithec
7	669	32.9	446	1	D3DR_MOUSE	P30728 mus musculu
8	657	32.3	463	1	D2DR_FUGRU	P53453 fugu rubrip
9	645	31.8	443	1	D2DR_HUMAN	P14416 homo sapien
10	644	31.7	443	1	D2DR_CERAE	P52702 cercopithec
11	636.5	31.3	444	1	D2DR_BOVIN	P20288 bos taurus
12	631.5	31.1	444	1	D2DR_MOUSE	P13953 mus musculu
13	629.5	31.0	442	1	D2D1_XENLA	P24628 xenopus lae
14	615	30.3	436	1	D2DR_MELGA	O73810 meleagris g
15	581	28.6	450	1	A2AA_PIG	P18871 sus scrofa
16	575	28.3	484	1	OAR2_LOCMI	Q25322 locusta mig
17	574.5	28.3	450	1	A2AB_HUMAN	P18089 homo sapien
18	574	28.3	448	1	A2AB_CAVPO	Q60475 cavia porce
19	573	28.2	484	1	OAR1_LOCMI	Q25321 locusta mig
20	565.5	27.8	461	1	A2AC_HUMAN	P18825 homo sapien
21	565	27.8	452	1	A2AA_BOVIN	Q28838 bos taurus
22	564	27.8	455	1	A2AC_CAVPO	Q60476 cavia porce
23	564	27.8	458	1	A2AD_HUMAN	P35369 homo sapien
24	563.5	27.7	455	1	A2AB_MOUSE	P30545 mus musculu
25	560.5	27.6	453	1	A2AB_RAT	P19328 rattus norv
26	559.5	27.5	379	1	GRE2_BALAM	Q93127 balanus amp
27	558	27.5	450	1	A2AA_HUMAN	P08913 homo sapien
28	554	27.3	458	1	A2AC_RAT	P22086 rattus norv
29	552.5	27.2	450	1	A2AA_CAVPO	Q60474 cavia porce
30	551	27.1	450	1	A2AA_MOUSE	Q01338 mus musculu
31	551	27.1	450	1	A2AA_RAT	P22909 rattus norv
32	547.5	27.0	458	1	A2AC_MOUSE	Q01337 mus musculu
33	542.5	26.7	422	1	5HIA_RAT	P19327 rattus norv
34	536.5	26.4	421	1	5HIA_MOUSE	Q64264 mus musculu
35	532.5	26.2	476	1	GRE1_BALAM	Q93126 balanus amp
36	529	26.0	601	1	OAR_DROME	P22270 drosophila
37	527	25.9	422	1	5HIA_HUMAN	P08908 homo sapien
38	522	25.7	432	1	A2AR_LABOS	Q91081 labrus ossi
39	521.5	25.7	473	1	B1AR_CANFA	P79148 canis famil
40	514.5	25.3	446	1	5HT_BOMMO	Q17239 bombyx mori
41	512.5	25.2	480	1	B1AR_MACMU	P47899 macaca mula
42	509.5	25.1	423	1	5HIA_FUGRU	O42385 fugu rubrip
43	508	25.0	400	1	B3AR_MOUSE	P25962 mus musculu
44	507	25.0	479	1	OAR_BOMMO	Q17232 bombyx mori
45	506	24.9	405	1	B3AR_CANFA	O02662 canis famil

ALIGNMENTS

RESULT 1
D4DR_HUMAN
ID D4DR_HUMAN STANDARD; PRT; 467 AA.
AC P21917;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).
GN DRD4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ALLELE D4.7).
RX MEDLINE=92310588; PubMed=1319557;
RA van Tol H.H., Wu C.M., Guan H.C., Ohara K., Bunzow J.R.,
RA Civelli O., Kennedy J., Seeman P., Niznik H.B., Jovanovic V.;
RT "Multiple dopamine D4 receptor variants in the human population.";
RL Nature 358:149-152(1992).
RN [2]
RP SEQUENCE FROM N.A. (ALLELE D4.2).
RC TISSUE=Brain;
RX MEDLINE=91204054; PubMed=1840645;
RA van Tol H.H.M., Bunzow J.R., Guan H.-C., Sunahara R.K., Seeman P.,
RA Niznik H.B., Civelli O.;
RT "Cloning of the gene for a human dopamine D4 receptor with high
RT affinity for the antipsychotic clozapine.";
RL Nature 350:610-614(1991).
RN [3]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=93038566; PubMed=1358063;
RA Livingstone C.D., Strange P.G., Naylor L.H.;
RT "Molecular modelling of D2-like dopamine receptors.";
RL Biochem. J. 287:277-282(1992).
RN [4]
RP VARIANT GLY-194.
RX MEDLINE=95243275; PubMed=7726213;
RA Seeman P., Ulpian C., Chouinard G., van Tol H.H.M., Dwosh H.,
RA Lieberman J.A., Siminovitch K., Liu I.S.C., Waye J., Voruganti P.,
RA Hudson C., Serjeant G.R., Masibay A.S., Seeman M.V.;
RT "Dopamine D4 receptor variant, D4-glycine-194, in Africans, but not in
RT Caucasians: no association with schizophrenia.";
RL Am. J. Med. Genet. 54:384-390(1994).
CC -!- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS
CC FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
CC PROTEINS WHICH INHIBIT ADENYLYL CYCLASE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- POLYMORPHISM: THE NUMBER OF REPEATS IS HIGHLY POLYMORPHIC AND
CC VARIES AMONG DIFFERENT ALLELES. THE SEQUENCE SHOWN IS THAT OF
CC ALLELE D4.7.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC ----------

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CC   ---------------------------------------------------------------------
DR   EMBL; L12398; AAB59386.1; -.
DR   EMBL; L12397; -; NOT_ANNOTATED_CDS.
DR   PIR; S15079; DYHUD4.
DR   GCRDb; GCR_0064; -.
DR   GCRDb; GCR_0571; -.
DR   MIM; 126452; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR00242; DOPAMINER.
DR   PRINTS; PR00569; DOPAMINED4R.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Polymorphism; Repeat.
FT   DOMAIN       1     37       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     38    60       1 (POTENTIAL).
FT   DOMAIN       61    70       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     71    93       2 (POTENTIAL).
FT   DOMAIN       94    109      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     110   131      3 (POTENTIAL).
FT   DOMAIN       132   151      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     152   175      4 (POTENTIAL).
FT   DOMAIN       176   191      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     192   213      5 (POTENTIAL).
FT   DOMAIN       214   394      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     395   417      6 (POTENTIAL).
FT   DOMAIN       418   426      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     427   449      7 (POTENTIAL).
FT   DOMAIN       450   467      CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       249   360      7 X 16 AA APPROXIMATE TANDEM REPEATS.
FT   REPEAT       249   264      1.
FT   REPEAT       265   280      2.
FT   REPEAT       281   296      3.
FT   REPEAT       297   312      4.
FT   REPEAT       313   328      5.
FT   REPEAT       329   344      6.
FT   REPEAT       345   360      7.
FT   CARBOHYD     3     3        N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID     108   185      BY SIMILARITY.
FT   VARIANT      194   194      V -> G (IN AFRO-CARRIBEANS).
FT                               /FTId=VAR_003464.
FT   VARIANT      265   344      MISSING (IN ALLELE D4.2).
FT                               /FTId=VAR_003465.
FT   VARIANT      281   328      MISSING (IN ALLELE D4.4).
FT                               /FTId=VAR_003466.
FT   VARIANT      329   329      P -> A (IN ALLELE D4.4).
FT                               /FTId=VAR_003467.
FT   VARIANT      332   332      G -> S (IN ALLELE D4.4).
FT                               /FTId=VAR_003468.
SQ   SEQUENCE   467 AA;  48360 MW;  B6FF2E09269A02AF CRC64;


  Query Match             97.3%;  Score 1976;  DB 1;  Length 467;
  Best Local Similarity   82.7%;  Pred. No. 5.3e-104;
  Matches  386;  Conservative    0;  Mismatches    1;  Indels   80;  Gaps    1;

Qy       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60

Qy      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVMLCT 120

Qy     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180

Qy     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240

Qy     241 PGPPSPTPPAPR---------------------------------------------- 252
           ||||||||||||
Db     241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPRGPCGPDCAPAAPGLPPDPCGPDCAPPAPG 300

Qy     253 ------------------------------LPQDPCGPDCAPPAPGLPPDPCGSNCAP 280
                                           ||||||||||||||||||||||||||||
Db     301 LPQDPCGPDCAPPAPGLPRGPCGPDCAPPAPGLPQDPCGPDCAPPAPGLPPDPCGSNCAP 360

Qy     281 PDAVRAAALPPQTPPQTRRRRRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALC 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 PDAVRAAALPPQTPPQTRRRRRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALC 420

Qy     341 PACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKALRACC 387
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     421 PACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKALRACC 467


RESULT   2
D4DR_MOUSE
ID   D4DR_MOUSE     STANDARD;      PRT;   387 AA.
AC   P51436; O35838;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).
GN   DRD4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV;
RX   MEDLINE=95212551; PubMed=7698326;
RA   Fishburn C.S., Carmon S., Fuchs S.;
RT   "Molecular cloning and characterisation of the gene encoding the
RT   murine D4 dopamine receptor.";
RL   FEBS Lett. 361:215-219(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96149998; PubMed=8584230;
RA   Suzuki T., Kobayashi K., Nagatsu T.;
RT   "Genomic structure and tissue distribution of the mouse dopamine D4
RT   receptor.";
RL   Neurosci. Lett. 199:69-72(1995).
CC   -!- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS
CC       FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
CC       PROTEINS WHICH INHIBIT ADENYLYL CYCLASE.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U19880; AAC52190.1; -.
DR   EMBL; S80929; AAB50730.1; -.
DR   EMBL; S80920; AAB50730.1; JOINED.
DR   EMBL; S80927; AAB50730.1; JOINED.
DR   EMBL; S80928; AAB50730.1; JOINED.
DR   HSSP; P29274; 1MMH.
DR   GCRDb; GCR_1706; -.
DR   MGD; MGI:94926; Drd4.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
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DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR00242; DOPAMINER.
DR   PRINTS; PR00569; DOPAMINED4R.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family.
FT   DOMAIN        1     34       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     35     57       1 (POTENTIAL).
FT   DOMAIN       58     67       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     68     90       2 (POTENTIAL).
FT   DOMAIN       91    106       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    107    128       3 (POTENTIAL).
FT   DOMAIN      129    146       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    147    170       4 (POTENTIAL).
FT   DOMAIN      171    186       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    187    208       5 (POTENTIAL).
FT   DOMAIN      209    314       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    315    337       6 (POTENTIAL).
FT   DOMAIN      338    346       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    347    369       7 (POTENTIAL).
FT   DOMAIN      370    387       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      3      3       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    105    180       BY SIMILARITY.
FT   CONFLICT     47     47       A -> T (IN REF. 2).
SQ   SEQUENCE   387 AA;  41486 MW;  BEA306D5E8AA02E9 CRC64;


  Query Match             74.3%;  Score 1510;  DB 1;  Length 387;
  Best Local Similarity   76.1%;  Pred. No. 4.6e-78;
  Matches  302;  Conservative   18;  Mismatches   57;  Indels   20;  Gaps    4;

Qy       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
           ||| |  :  ||||||||    | |  ||| | ||||||||||||| ||||||||||||
Db       1 MGNSSATEDGGLLAGRGP---ESLGTGAGLGGAGAAALVGGVLLIGLVLAGNSLVCVSVA 57

Qy      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
           :|| |||||| |||||||||||||:||||||||||||| ||||||||| |||||| |||
Db      58 SERTLQTPTNYFIVSLAAADLLLAVLVLPLFVYSEVQGGVWLLSPRLCDTLMAMDVMLCT 117

Qy     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
           |||||||||||||||| ||||||:||  : ||||| ||||||||||:||:|||||| ||
Db     118 ASIFNLCAISVDRFVAVTVPLRYNQQG--QCQLLLIAATWLLSAAVASPVVCGLNDVPGR 175

Qy     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
           ||||| ||:|||||||||||||||||||||||||||||||:||| ||  ||| ||||||||
Db     176 DPAVCCLENRDYVVYSSVCSFFLPCPLMLLLYWATFRGLRRWEAARHTKLHSRAPRRPSG 235

Qy     241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSN----------CAPPDAVRAAALP 290
           ||||   |      | |  ||| || | |   |  |:          |:|   :  ||||
Db     236 PGPPVSDP-----TQGPFFPDCPPPLPSLRTSPSDSSRPESELSQRPCSPGCLLADAALP 290

Qy     291 PQTPPQTRRRRRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLV 350
             | :|||| ||||||||||||||||||||:||||||||||:|||||| | ||||
Db     291 QPPEPSSRRRRGAKITGRERKAMRVLPVVVGAFLVCWTPFFVVHITRALCPACFVSPRLV 350

Qy     351 SAVTWLGYVNSALNPVIYTVFNAEFRNVFRKALRACC 387
           |||||||||||||:|||:||||||:|||| ||  |
Db     351 SAVTWLGYVNSALNPIIYTIFNAEFRSVFRKTLRLRC 387


RESULT   3
D4DR_RAT
ID   D4DR_RAT       STANDARD;      PRT;   387 AA.
AC   P30729; Q62610;
DT   01-APR-1993 (Rel. 25, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).
GN   DRD4.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92207907; PubMed=1554689;
RA   O'Malley K.L., Harmon S., Tang L., Todd R.D.;
RT   "The rat dopamine D4 receptor: sequence, gene structure, and
RT   demonstration of expression in the cardiovascular system.";
RL   New Biol. 4:137-146(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Asghari V., Schoots O., Van Kats S., Ohara K., Jovanovic V.,
RA   Guan H., Bunzow J.R., Petronis A., Van Tol H.H.M.;
RT   "The dopamine D4 receptor repeat: analysis of different native and
RT   mutant forms of the human and rat gene.";
RL   Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS
CC       FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
CC       PROTEINS WHICH INHIBIT ADENYLYL CYCLASE.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM: HYPOTHALAMUS,
CC       THALAMUS, OLFACTORY BULB, AND FRONTAL CORTEX.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ----------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M84009; AAA96716.1; -.
DR   EMBL; U03551; AAA18588.1; -.
DR   HSSP; P29274; 1MMH.
DR   GCRDb; GCR_0279; -.
DR   GCRDb; GCR_1032; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR00242; DOPAMINER.
DR   PRINTS; PR00569; DOPAMINED4R.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family.
FT   DOMAIN        1     34       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     35     57       1 (POTENTIAL).
FT   DOMAIN       58     67       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     68     90       2 (POTENTIAL).
FT   DOMAIN       91    106       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    107    128       3 (POTENTIAL).
FT   DOMAIN      129    146       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    147    170       4 (POTENTIAL).
FT   DOMAIN      171    186       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    187    208       5 (POTENTIAL).
FT   DOMAIN      209    314       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    315    337       6 (POTENTIAL).
FT   DOMAIN      338    346       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    347    369       7 (POTENTIAL).
FT   DOMAIN      370    387       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      3      3       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    105    180       BY SIMILARITY.
FT   CONFLICT     93     94       MISSING (IN REF. 1).
SQ   SEQUENCE   387 AA;  41294 MW;  1E0A5D74524F5050 CRC64;


  Query Match             73.7%;  Score 1496;  DB 1;  Length 387;
  Best Local Similarity   75.1%;  Pred. No. 2.8e-77;
  Matches  301;  Conservative   15;  Mismatches   57;  Indels   28;  Gaps    6;

Qy       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
           ||| |     ||||||||    | |   || | |||||||||||||| ||||||||||||
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Db       1 MGNSSATGDGGLLAGRGP---ESLGTGTGLGGAGAAALVGGVLLIGMVLAGNSLVCVSVA 57

Qy      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
           :|| |||||| |||||||||||||:||||||||||||||| |||||||||| |||||| |||
Db      58 SERILQTPTNYFIVSLAAADLLLAVLVLPLFVYSEVQGGVWLLSPRLCDTLMAMDVMLCT 117

Qy     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
           |||||||||||||||| |||||:||  : ||||| |||||||||||||:||||||| ||
Db     118 ASIFNLCAISVDRFVAVTVPLRYNQQG--QCQLLLIAATWLLSAAVAAPVVCGLNDVPGR 175

Qy     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
           || || |||||||||||:|||||||||||||||||||||:||| ||  ||| ||||||||
Db     176 DPTVCCLEDRDYVVYSSICSFFLPCPLMLLLYWATFRGLRRWEAARHTKLHSRAPRRPSG 235

Qy     241 PGPPSPTPPAPRLPQDPCGPDCAPPAPG-------------LPPDPCGSNCAPPDAVRA 286
           ||||   |      | |   || ||:|                |   ||   |  ||| |
Db     236 PGPPVSDP-----TQGPLFSDCPPPSPSLRTSPTVSSRPESDLSQSPCSPGCLLPDA--A 288

Qy     287 AALPPQTPPQTRRRRRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVP 346
           | ||   | :||:| ||||||||||||||||||||:||||||||||:|||||| |
Db     289 LAQPP--APSSRRKRGAKITGRERKAMRVLPVVVGAFLMCWTPFFVVHITRALCPACFVS 346

Qy     347 PRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKALRACC 387
           |||||||||||||||||:|||:||||||:|||| ||  |
Db     347 PRLVSAVTWLGYVNSALNPIIYTIFNAEFRSVFRKTLRLRC 387
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RESULT   4
D3DR_RAT
ID   D3DR_RAT       STANDARD;      PRT;   446 AA.
AC   P19020; P70647;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   D(3) DOPAMINE RECEPTOR.
GN   DRD3.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY;
RX   MEDLINE=90370111; PubMed=1975644;
RA   Sokoloff P., Giros B., Martres M.-P., Bouthenet M.-L., Schwartz J.-C.;
RT   "Molecular cloning and characterization of a novel dopamine receptor
RT   (D3) as a target for neuroleptics.";
RL   Nature 347:146-151(1990).
RN   [2]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX   MEDLINE=91248260; PubMed=2039532;
RA   Giros B., Martres M.-P., Pilon C., Sokoloff P., Schwartz J.-C.;
RT   "Shorter variants of the D3 dopamine receptor produced through
RT   various patterns of alternative splicing.";
RL   Biochem. Biophys. Res. Commun. 176:1584-1592(1991).
RN   [3]
RP   SEQUENCE OF 71-106 FROM N.A.
RX   MEDLINE=93326159; PubMed=8333859;
RA   Pagliusi S., Chollet-Daemerius A., Losberger C., Mills A.,
RA   Kawashima E.;
RT   "Characterization of a novel exon within the D3 receptor gene giving
RT   rise to an mRNA isoform expressed in rat brain.";
RL   Biochem. Biophys. Res. Commun. 194:465-471(1993).
RN   [4]
RP   3D-STRUCTURE MODELING.
RC   TISSUE=Brain;
RX   MEDLINE=93038566; PubMed=1358063;
RA   Livingstone C.D., Strange P.G., Naylor L.H.;
RT   "Molecular modelling of D2-like dopamine receptors.";
RL   Biochem. J. 287:277-282(1992).
CC   -!- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS
CC       FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
CC       PROTEINS WHICH INHIBIT ADENYLYL CYCLASE.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- TISSUE SPECIFICITY: MAINLY IN LIMBIC AREAS OF BRAIN.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X53944; CAA37887.1; -.
DR   EMBL; M69194; AAA41076.1; ALT_SEQ.
DR   EMBL; M69189; AAA41076.1; JOINED.
DR   EMBL; M69190; AAA41076.1; JOINED.
DR   EMBL; M69191; AAA41076.1; JOINED.
DR   EMBL; M69192; AAA41076.1; JOINED.
DR   EMBL; M69193; AAA41076.1; JOINED.
DR   EMBL; A17751; CAA01349.1; -.
DR   EMBL; A17753; CAA01350.1; -.
DR   EMBL; S63847; AAB27545.1; -.
DR   EMBL; S63846; AAB27545.1; JOINED.
DR   PIR; S11565; DYRTD3.
DR   GCRDb; GCR_0134; -.
DR   GCRDb; GCR_0221; -.
DR   GCRDb; GCR_0236; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR00242; DOPAMINER.
DR   PRINTS; PR00568; DOPAMINED3R.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Alternative splicing.
FT   DOMAIN       1     32       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    33     55       1 (POTENTIAL).
FT   DOMAIN      56     66       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    67     92       2 (POTENTIAL).
FT   DOMAIN      93    104       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   105    126       3 (POTENTIAL).
FT   DOMAIN     127    149       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   150    172       4 (POTENTIAL).
FT   DOMAIN     173    185       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   186    209       5 (POTENTIAL).
FT   DOMAIN     210    375       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   376    397       6 (POTENTIAL).
FT   DOMAIN     398    412       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   413    434       7 (POTENTIAL).
FT   DOMAIN     435    446       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    12     12       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    19     19       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    97     97       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   173    173       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID   103    181       BY SIMILARITY.
FT   VARSPLIC    92    100       TGGVWNFSR -> HSGGHASSL (IN ISOFORM
FT                               D3(TM3-DEL)).
FT   VARSPLIC   101    446       MISSING (IN ISOFORM D3(TM3-DEL)).
FT   VARSPLIC   176    193       MISSING (IN ISOFORM D3(O2-DEL)).
FT   CONFLICT    71     71       L -> M (IN REF. 3).
FT   CONFLICT   139    139       Q -> E (IN REF. 2).
SQ   SEQUENCE   446 AA;  49515 MW;  180E36AFF217E9DB CRC64;
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  Query Match             33.6%;  Score 683;  DB 1;  Length 446;
  Best Local Similarity   37.4%;  Pred. No. 7.3e-32;
  Matches  154;  Conservative   54;  Mismatches  126;  Indels   78;  Gaps    8;

Qy      44 LIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLL 103
           || |:: || ||| :|  |||||| ||  :|||| ||||:| ||:|  || || || |
Db      39 LILAIIFGNGLVCAAVLRERALQTTTNYLVVSLAVADLLVATLVMPWVVYLEVTGGVWNF 98
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Qy     104 SPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYNR---QGGSRRQLLLIGATW 160
           |   ||  : :|| :|||||| |||||||:||: || :|: |      |   ||  |:| | |
Db      99 SRICCDVFVTLDVMMCTASILNLCAISIDRYTAVVMPVHYQHGTGQSSCRRVALMITAVW 158

Qy     161 LLSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLY---WATFR 217
           :|: ||: |:| | |     ||::| : : |:|:|||| ||::|  : :|:|   :   |
Db     159 VLAFAVSCPLLFGFNTT--GDPSICSISNPDFVIYSSVVSFYVPFGVTVLVYARIYIVLR 216

Qy     218 GLQRWEVARRAKLHGRAPRRPSGPGPPSPT---------------------------- 247
             ||  :  |      : |    || |  :
Db     217 QRQRKRILTRQNSQCISIR----PGFPQQSSCLRLHPIRQFSIRARFLSDATGQMEHIED 272

Qy     248 PPAPRLPQDPCGPDCAPPAPGL------------------PPDPCGSNCAPPDAVRAAA 288
             |:  |||      ||:||                    |    |:  :| :  | :
Db     273 KQYPQKCQDPLLSHLQPPSPGQTHGGLKRYYSICQDTALRHPSLEGGAGMSPVERTRNSL 332

Qy     289 LPPQTPP---QTRRRRRAKITG--------------RERKAMRVLPVVVGAFLLCWTPFF 331
           |   |    : |:    :::                ||:|| ::: :|:|||::|| |||
Db     333 SPTMAPKLSLEVRKLSNGRLSTSLRLGPLQPRGVPLREKKATQMVVIVLGAFIVCWLPFF 392

Qy     332 VVHITQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKAL 383
           : |:    | || | | |  | ||||||||||||||| || |||  | | |
Db     393 LTHVLNTHCQACHVSPELYRATTWLGYVNSALNPVIYTTFNVEFRKAFLKIL 444


RESULT  5
D3DR_HUMAN
ID   D3DR_HUMAN     STANDARD;      PRT;   400 AA.
AC   P35462;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   D(3) DOPAMINE RECEPTOR.
GN   DRD3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (D3).
RX   MEDLINE=91274966; PubMed=2129115;
RA   Giros B., Martres M.-P., Sokoloff P., Schwartz J.-C.;
RT   "Gene cloning of human dopaminergic D3 receptor and identification of
RT   its chromosome.";
RL   C. R. Acad. Sci., III, Sci. Vie 311:501-508(1990).
RN   [2]
RP   SEQUENCE FROM N.A. (D3).
RA   Fishburn C.S., Park B.-H., Fuchs S.;
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (D3NF).
RC   TISSUE=Brain;
RX   MEDLINE=94022291; PubMed=8415635;
RA   Schmauss C., Haroutunian V., Davis K.L., Davidson M.;
RT   "Selective loss of dopamine D3-type receptor mRNA expression in
RT   parietal and motor cortices of patients with chronic schizophrenia.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:8942-8946(1993).
RN   [4]
RP   ALTERNATIVE SPLICING.
RC   TISSUE=Brain;
RX   MEDLINE=95050745; PubMed=7961889;
RA   Liu K., Bergson C., Levenson R., Schmauss C.;
RT   "On the origin of mRNA encoding the truncated dopamine D3-type
RT   receptor D3nf and detection of D3nf-like immunoreactivity in human
RT   brain.";
RL   J. Biol. Chem. 269:29220-29226(1994).
RN   [5]
RP   VARIANT GLY-9.
RA   Lannfelt T., Sokoloff P., Martres M.-P., Pilon C., Giros B.,
RA   Joensson E., Sedvall G., Schwartz J.-C.;
RT   "Amino-acid substitution in the dopamine D3 receptor as useful
RT   polymorphism for investigating psychiatric disorders.";
RL   Psychiatr. Genet. 2:249-256(1992).
RN   [6]
RP   VARIANT GLY-9.
RX   MEDLINE=97186429; PubMed=9034004;
RA   Chen C.-H., Liu M.-Y., Wei F.-C., Koong F.-J., Hwu H.-G., Hsiao K.-J.;
RT   "Further evidence of no association between Ser9Gly polymorphism of
RT   dopamine D3 receptor gene and schizophrenia.";
RL   Am. J. Med. Genet. 74:40-43(1997).
CC   -!- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS
CC       FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
CC       PROTEINS WHICH INHIBIT ADENYLYL CYCLASE.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; D3 (SHOWN HERE) AND D3NF;
CC       ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: BRAIN.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L20469; AAA03543.1; -.
DR   EMBL; U32499; AAA73929.1; -.
DR   EMBL; L35903; AAA64369.1; ALT_SEQ.
DR   EMBL; L35902; AAA64369.1; JOINED.
DR   EMBL; A19667; CAA01483.1; -.
DR   GCRDb; GCR_0699; -.
DR   GCRDb; GCR_0936; -.
DR   GCRDb; GCR_1869; -.
DR   GCRDb; GCR_1975; -.
DR   MIM; 126451; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR00242; DOPAMINER.
DR   PRINTS; PR00568; DOPAMINED3R.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Alternative splicing; Polymorphism.
FT   DOMAIN       1     32       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    33     55       1 (POTENTIAL).
FT   DOMAIN      56     66       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    67     92       2 (POTENTIAL).
FT   DOMAIN      93    104       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   105    126       3 (POTENTIAL).
FT   DOMAIN     127    149       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   150    172       4 (POTENTIAL).
FT   DOMAIN     173    185       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   186    209       5 (POTENTIAL).
FT   DOMAIN     210    329       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   330    351       6 (POTENTIAL).
FT   DOMAIN     352    366       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   367    388       7 (POTENTIAL).
FT   DOMAIN     389    400       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    12     12       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    19     19       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    97     97       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   173    173       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID   103    181       BY SIMILARITY.
FT   VARSPLIC   288    400       PTIAPKLSLEVRKLSNGRLSTSLKLGPLQPRGVPLREKKAT
FT                               QMVAIVLGAFIVCWLPFFLTHVLNTHCQTCHVSPELYSATT
FT                               WLGYVNSALNPVIYTTFNIEFRKAFLKILSC -> ATSGEE
FT                               GNPNGGHCAWGLHCLLAALLLDPCSQYPLPDMPRVPRALQC
FT                               HDMAGLRE (IN ISOFORM D3NF).
FT   VARIANT      9      9       S -> G.
FT                               /FTId=VAR_003463.
SQ   SEQUENCE   400 AA;  44224 MW;  2CDA789D78378DDA CRC64;
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  Query Match             33.4%;  Score 679;  DB 1;  Length 400;
  Best Local Similarity   38.8%;  Pred. No. 1.1e-31;
  Matches  155;  Conservative   51;  Mismatches  141;  Indels   52;  Gaps    8;

Qy      21 GASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAAD 80
           ||      |  |   |   :    || |:: || |||::|  |||||| ||  :|||| ||
Db      16 GAENSTGASQARPHAYYALSYCALILAIVFGNGLVCMAVLKERALQTTTNYLVVSLAVAD 75

Qy      81 LLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVP 140
           ||:| ||:|  || || || |  |   ||  : :|| :|||| |||||:||: ||, :|
Db      76 LLVATLVMPWVVYLEVTGGVWNFSRICCDVFVTLDVMMCTASILNLCAISIDRYTAVVMP 135

Qy     141 LRYNR---QGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSS 197
           : |     |   ||  |:| | |:|: ||: |:| | |     || || : : |:|:|||
Db     136 VHYQHGTGQSSCRRVALMITAVWVLAFAVSCPLLFGFNTT--GDPTVCSISNPDFVIYSS 193

Qy     198 VCSFFLPCPLMLLLY---WATFRGLQRWEVARRAKLHGRAPRRPSGPGPPSPTPPAPRLP 254
           | ||:||  : :|:|   :   :  :|  :  |      : |              | |
Db     194 VVSFYLPFGVTVLVYARIYVVLKQRRRKRILTRQNSQCNSVR----------PGFP 239

Qy     255 QDPCGPD----------CAPPAPGLPP-DPCGSNCAPPDAVRAAALP---PQTPPQTR 298
           |    ||           |  | | |      :  | :  |   |:   : |
Db     240 QQTLSPDPAHLELKRYYSICQDTALGGPGFQERGGELKREEKTRNSLSPTIAPKLSLEVR 299

Qy     299 RRRRAKITG----------RERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACS 344
           :   :::              ||:|| ::: :|:|||::|| |||: |:    |  |
Db     300 KLSNGRLSTSLKLGPLQPRGVPLREKKATQMVAIVLGAFIVCWLPFFLTHVLNTHCQTCH 359

Qy     345 VPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKAL 383
           | | | || ||||||||||||||| || |||  | | |
Db     360 VSPELYSATTWLGYVNSALNPVIYTTFNIEFRKAFLKIL 398


RESULT   6
D3DR_CERAE
ID   D3DR_CERAE     STANDARD;      PRT;   400 AA.
AC   P52703;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   D(3) DOPAMINE RECEPTOR.
GN   DRD3.
OS   Cercopithecus aethiops (Green monkey) (Grivet).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercopithecus.
OX   NCBI_TaxID=9534;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Ross P.C.;
RL   Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS
CC       FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
CC       PROTEINS WHICH INHIBIT ADENYLYL CYCLASE.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U21307; AAA75379.1; -.
DR   GCRDb; GCR_1207; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR00242; DOPAMINER.
DR   PRINTS; PR00568; DOPAMINED3R.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family.
FT   DOMAIN        1     32       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      33    55       1 (POTENTIAL).
FT   DOMAIN        56    66       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      67    92       2 (POTENTIAL).
FT   DOMAIN        93    104      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      105   126      3 (POTENTIAL).
FT   DOMAIN        127   149      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      150   172      4 (POTENTIAL).
FT   DOMAIN        173   185      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      186   209      5 (POTENTIAL).
FT   DOMAIN        210   329      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      330   351      6 (POTENTIAL).
FT   DOMAIN        352   366      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      367   388      7 (POTENTIAL).
FT   DOMAIN        389   400      CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      12    12       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      19    19       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      97    97       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      173   173      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID      103   181      BY SIMILARITY.
SQ   SEQUENCE   400 AA;  44336 MW;  9358843CB0BA698B CRC64;


  Query Match             33.2%;  Score 675;  DB 1;  Length 400;
  Best Local Similarity   39.9%;  Pred. No. 1.9e-31;
  Matches  150;  Conservative   50;  Mismatches  124;  Indels   52;  Gaps    8;

Qy      44 LIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLL 103
           || |:: || |||::|  |||||| ||  :|||| ||||:| ||:|  || || || |
Db      39 LILAIVFGNGLVCMAVLKERALQTTTNYLVVSLAVADLLVATLVMPWVVYLEVTGGVWNF 98

Qy     104 SPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYNR---QGGSRRQLLLIGATW 160
           |   ||  : :|| :||||| ||||||:||: || :|: |     |   ||  |:| | |
Db      99 SRVCCDVFVTLDVMMCTASILNLCAISIDRYTAVVMPVHYQHGTGQSSCRRVTLMITAVW 158

Qy     161 LLSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLY---WATFR 217
           :|: ||: |:| | |     || || : : |:|:|||| ||:||  : :|:|   :   :
Db     159 VLAFAVSCPLLFGFNTT--GDPTVCSISNPDFVIYSSVVSFYLPFGVTVLVYARIYVVLK 216

Qy     218 GLQRWEVARRAKLHGRAPRRPSGPGPPSPTPPAPRLPQDPCGPD----------CAPP 265
             :|  :  |      : |              | ||    ||            |
Db     217 QRRRKRILTRQNSQCNSVR----------PGFPQQTLSPDRAHLELKRYYSICQDT 262

Qy     266 APGLPP-DPCGSNCAPPDAVRAAALP---PQTPPQTRRRRRAKITG---------- 307
           | | |      |     :  | :  |   |:    : |:    :::
Db     263 ALGGPGFQERGGELKREERTRNSLSPTIAPKLSLEVRKLSNGRLSTSLKLGPLQPRGVPL 322

Qy     308 RERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVNSALNPVI 367
           ||:|| ::: :|:|||::|| |||: |:    |  | | | | || ||||||||||||||
Db     323 REKKATQMVAIVLGAFIVCWLPFFLTHVLNTHCQTCHVSPELYSATTWLGYVNSALNPVI 382

Qy     368 YTVFNAEFRNVFRKAL 383
           || || |||  | | |
Db     383 YTTFNIEFRKAFLKIL 398


RESULT   7
D3DR_MOUSE
ID   D3DR_MOUSE     STANDARD;      PRT;   446 AA.
AC   P30728;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   D(3) DOPAMINE RECEPTOR.
GN   DRD3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
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RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Fishburn C.S., David C., Carmon S., Belleli D., Fuchs S.;
RL   Submitted (JUL-1992) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95322026; PubMed=7598803;
RA   Fu D., Skryabin B.V., Brosius J., Robakis N.K.;
RT   "Molecular cloning and characterization of the mouse dopamine D3
RT   receptor gene: an additional intron and an mRNA variant.";
RL   DNA Cell Biol. 14:485-492(1995).
CC   -!- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS
CC       FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
CC       PROTEINS WHICH INHIBIT ADENYLYL CYCLASE.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; D3LONG (SHOWN HERE) AND D3SHORT;
CC       ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X67274; CAA47691.1; -.
DR   EMBL; S78580; AAB35066.2; -.
DR   EMBL; S78574; AAB35066.2; JOINED.
DR   EMBL; S78638; AAB35066.2; JOINED.
DR   EMBL; S78577; AAB35066.2; JOINED.
DR   EMBL; S78578; AAB35066.2; JOINED.
DR   EMBL; S78579; AAB35066.2; JOINED.
DR   EMBL; S78639; AAB35066.2; JOINED.
DR   PIR; S25161; S25161.
DR   GCRDb; GCR_0449; -.
DR   MGD; MGI:94925; Drd3.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR00242; DOPAMINER.
DR   PRINTS; PR00568; DOPAMINED3R.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Alternative splicing.
FT   DOMAIN        1     32       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     33     55       1 (POTENTIAL).
FT   DOMAIN       56     66       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     67     92       2 (POTENTIAL).
FT   DOMAIN       93    104       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    105    126       3 (POTENTIAL).
FT   DOMAIN      127    149       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    150    172       4 (POTENTIAL).
FT   DOMAIN      173    185       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    186    209       5 (POTENTIAL).
FT   DOMAIN      210    375       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    376    397       6 (POTENTIAL).
FT   DOMAIN      398    412       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    413    434       7 (POTENTIAL).
FT   DOMAIN      435    446       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     12     12       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     19     19       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     97     97       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    173    173       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    103    181       BY SIMILARITY.
FT   VARSPLIC    268    288       MISSING (IN ISOFORM D3SHORT).
SQ   SEQUENCE   446 AA;  49669 MW;  B391C2D493B58242 CRC64;

  Query Match             32.9%;  Score 669;  DB 1;  Length 446;
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  Best Local Similarity   37.2%;  Pred. No. 4.4e-31;
  Matches  153;  Conservative   54;  Mismatches  128;  Indels   76;  Gaps    8;

Qy      44 LIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLL 103
           || |:: || ||| :|  |||||| ||  :|||| ||||:| ||:|  || || || |
Db      39 LILAIIFGNGLVCAAVLRERALQTTTNYLVVSLAVADLLVATLVMPWVVYLEVTGGVWNF 98

Qy     104 SPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYNR---QGGSRRQLLLIGATW 160
           |   ||  : :|| :|||| |||||:||: || :|: |     |   ||  |:| | |
Db      99 SRICCDVFVTLDVMMCTASILNLCAISIDRYTAVVMPVHYQHGTGQSSCRRVALMITAVW 158

Qy     161 LLSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQ 220
           :|: ||: |:| | |     ||::| : : |:|:|||| ||::|  : :|:|   :  |:
Db     159 VLAFAVSCPLLFGFNTT--GDPSICSISNPDFVIYSSVVSFYVPFGVTVLVYARIYMVLR 216

Qy     221 RWEVARRAKLHGRAPR-----RPSGPGPPS--------------------------PTP 248
           :    || ::  |         ||  |   |
Db     217 Q---RRRKRILTRQNSQCISIRPGFPQQSSCLRLHPIRQFSIRARFLSDATGQMEHIEDK 273

Qy     249 PAPRLPQDPCGPDCAPPAPGL------------------PPDPCGSNCAPPDAVRAAAL 289
           | |:  |||       | :||                    |   |   :  :  | :
Db     274 PYPQKCQDPLLSHLQPLSPGQTHGELKRYYSICQDTALRHPNFEGGGGMSQVERTRNSLS 333

Qy     290 PPQTPP---QTRRRRRAKITG-------------RERKAMRVLPVVVGAFLLCWTPFFV 332
           |   |    : |:    :::               ||:|| ::: :|:|||::|| |||:
Db     334 PTMAPKLSLEVRKLSNGRLSTSLKLGPLQPRGVPLREKKATQMVVIVLGAFIVCWLPFFL 393

Qy     333 VHITQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKAL 383
           |:    | || | | |  | ||||||||||||||| || |||  | | |
Db     394 THVLNTHCQACHVSPELYRATTWLGYVNSALNPVIYTTFNIEFRKAFLKIL 444

RESULT   8
D2DR_FUGRU
ID   D2DR_FUGRU     STANDARD;      PRT;   463 AA.
AC   P53453;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   D(2)-LIKE DOPAMINE RECEPTOR.
GN   D215.
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95309911; PubMed=7789977;
RA   Machae A.D., Brenner S.;
RT   "Analysis of the dopamine receptor family in the compact genome of
RT   the puffer fish Fugu rubripes.";
RL   Genomics 25:436-446(1995).
CC   -!- FUNCTION: RECEPTOR FOR DOPAMINE.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X80175; CAA56456.1; -.
DR   GCRDb; GCR_1107; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR00242; DOPAMINER.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
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DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family.
FT   DOMAIN        1     35       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     36     58       1 (POTENTIAL).
FT   DOMAIN       59     69       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     70     95       2 (POTENTIAL).
FT   DOMAIN       96    106       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    107    128       3 (POTENTIAL).
FT   DOMAIN      129    149       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    150    172       4 (POTENTIAL).
FT   DOMAIN      173    187       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    188    211       5 (POTENTIAL).
FT   DOMAIN      212    392       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    393    416       6 (POTENTIAL).
FT   DOMAIN      417    425       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    426    449       7 (POTENTIAL).
FT   DOMAIN      450    463       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     10     10       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     16     16       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     22     22       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    105    183       BY SIMILARITY.
SQ   SEQUENCE   463 AA;  52120 MW;  A54B178D7718AF6B CRC64;


  Query Match             32.3%;  Score 657;  DB 1;  Length 463;
  Best Local Similarity   35.4%;  Pred. No. 2.1e-30;
  Matches  151;  Conservative   64;  Mismatches  121;  Indels   90;  Gaps    8;

Qy      43 LLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWL 102
           |||  :: || |||:|: |:|||| ||  ||||| ||||:| ||:|  || ||  | |
Db      41 LLIFVIVFGNVLVCMAVSREKALQTTTNYLIVSLAVADLLVATLVMPWVVYLEVV-GEWR 99

Qy     103 LSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQL-LLIGATWL 161
             |   ||  : :|| :||||| ||||||:||: |||:|: || :  |||:: ::|   |:
Db      100 FSKIHCDIFVTLDVMMCTASILNLCAISIDRYTAVAMPMLYNTRYSSRRRVTVMISVVWV 159

Qy     162 LSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQR 221
           || |:: |:| |||:   || ::| : :  :|||||: ||::|  : ||:|   :  |::
Db      160 LSFAISCPLLFGLNNTATRDQSLCFIANPAFVVYSSIVSFYVPFIVTLLVYVQIYVVLRK 219

Qy     222 WEVARRAKLHGRAPRR---PSGPGPPSPTPPAPRLPQDP---------------------- 257
               || ::: :  :|    : |  |:         |:|
Db      220 ----RRKRVNTKPKQRLCQAADPDIPTSLKDKCTHPEDVRLCTMIVKSNGSFPVNKKKVI 275

Qy     258 -------------------CGPDCAPPAPGLPPDPCGSNCAPPD----AVRAAALP---P 291
                             ||     | |   |   |   |       : :| | |   |
Db      276 FIKDGVNEVEGLELDELNYCGGSHKQPPPQQQPRALGDTPATSHQLLMSTKANASPTSTP 335

Qy     292 QTPPQTRRR---------------------------------RRAKITGRERKAMRVLP 317
           |||:  :|                                  :|     :|:|| ::|
Db      336 PTPPEEGQRTEKNGDPTKEAQGNPAPVVALRNGKTQTSLKTLSKRKISQQKEKKATQMLA 395

Qy     318 VVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRN 377
           :|:| |::|| ||| ||    |  | ||  : :| |||||||||:||:||| || |||
Db      396 IVLGVFIICWLPFFITHILNTHCTRCKVPAEMYNAFTWLGYVNSAVNPIIYTTFNVEFRK 455

Qy     378 VFRKAL 383
           | | |
Db      456 AFIKIL 461


RESULT   9
D2DR_HUMAN
ID   D2DR_HUMAN     STANDARD;      PRT;   443 AA.
AC   P14416;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   D(2) DOPAMINE RECEPTOR.
GN   DRD2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90126238; PubMed=2533064;
RA   Selbie L.A., Hayes G., Shine J.;
RT   "The major dopamine D2 receptor: molecular analysis of the human D2A
RT   subtype.";
RL   DNA 8:683-689(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90076122; PubMed=2531656;
RA   Dal-Toso R., Sommer B., Ewert M., Herb A., Pritchett D.B., Bach A.,
RA   Shivers B.D., Seeburg P.H.;
RT   "The dopamine D2 receptor: two molecular forms generated by
RT   alternative splicing.";
RL   EMBO J. 8:4025-4034(1989).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Retina;
RX   MEDLINE=90206805; PubMed=2138729;
RA   Robakis N.K., Mohamadi M., Fu D.Y., Sambamurti K., Refolo L.M.;
RT   "Human retina D2 receptor cDNAs have multiple polyadenylation sites
RT   and differ from a pituitary clone at the 5' non-coding region.";
RL   Nucleic Acids Res. 18:1299-1299(1990).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90099344; PubMed=2532362;
RA   Grandy D.K., Marchionni M.A., Makam H., Stofko R.E., Alfano M.,
RA   Frothingham L., Fischer J.B., Burke-Howie K.J., Bunzow J.R.,
RA   Server A.C., Civelli O.;
RT   "Cloning of the cDNA and gene for a human D2 dopamine receptor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:9762-9766(1989).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Retina;
RX   MEDLINE=90136534; PubMed=2137193;
RA   Stormann T.M., Gdula D.C., Weiner D.M., Brann M.R.;
RT   "Molecular cloning and expression of a dopamine D2 receptor from
RT   human retina.";
RL   Mol. Pharmacol. 37:1-6(1990).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91000955; PubMed=2144985;
RA   Selbie L.A., Hayes G., Shine J.;
RT   "DNA homology screening: isolation and characterization of the human
RT   D2A dopamine receptor subtype.";
RL   Adv. Second Messenger Phosphoprotein Res. 24:9-14(1990).
RN   [7]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93264902; PubMed=1363862;
RA   Araki K., Kuwano R., Morii K., Hayashi S., Minoshima S.,
RA   Shimizu N., Katagiri T., Usui H., Kumanishi T., Takahashi Y.;
RT   "Structure and expression of human and rat D2 dopamine receptor
RT   genes.";
RL   Neurochem. Int. 21:91-98(1992).
RN   [8]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92076439; PubMed=1835903;
RA   Dearry A., Falardeau P., Shores C., Caron M.G.;
RT   "D2 dopamine receptors in the human retina: cloning of cDNA and
RT   localization of mRNA.";
RL   Cell. Mol. Neurobiol. 11:437-453(1991).
RN   [9]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=93228763; PubMed=8471125;
RA   Seeman P., Ohara K., Ulpian C., Seeman M.V., Jellinger K.,
RA   Tol H.H., Niznik H.B.;
RT   "Schizophrenia: normal sequence in the dopamine D2 receptor region
RT   that couples to G-proteins. DNA polymorphisms in D2.";
RL   Neuropsychopharmacology 8:137-142(1993).
RN   [10]
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RP   VARIANT CYS-311.
RX   MEDLINE=94071899; PubMed=7902708;
RA   Itokawa M., Arinami T., Futamura N., Hamaguchi H., Toru M.;
RT   "A structural polymorphism of human dopamine D2 receptor, D2(Ser311--
RT   >Cys).";
RL   Biochem. Biophys. Res. Commun. 196:1369-1375(1993).
CC   -!- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS
CC       FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
CC       PROTEINS WHICH INHIBIT ADENYLYL CYCLASE.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC       SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- DISEASE: IT HAS BEEN SUGGESTED THAT DRD2 IS INVOLVED IN
CC       PSYCHIATRIC DISORDERS; ESPECIALLY IN SCHIZOPHRENIA. IT HAS ALSO
CC       BEEN IMPLICATED IN SUSCEPTIBILITY TO ALCOHOLISM.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M30625; AAA88024.1; -.
DR   EMBL; X51645; CAB56463.1; -.
DR   EMBL; X51646; CAB37869.1; -.
DR   EMBL; X51362; CAA35746.1; -.
DR   EMBL; M29066; AAA52761.1; -.
DR   EMBL; S62137; AAB26819.1; -.
DR   EMBL; S69899; AAB20571.1; -.
DR   EMBL; S58589; AAB26274.1; -.
DR   EMBL; S58577; AAB26274.1; JOINED.
DR   EMBL; S58584; AAB26274.1; JOINED.
DR   EMBL; S58586; AAB26274.1; JOINED.
DR   EMBL; S58588; AAB26274.1; JOINED.
DR   PIR; S08417; DYHUD2.
DR   PIR; A37384; A37384.
DR   GCRDb; GCR_0063; -.
DR   GCRDb; GCR_0065; -.
DR   GCRDb; GCR_0066; -.
DR   GCRDb; GCR_0307; -.
DR   GCRDb; GCR_0310; -.
DR   GCRDb; GCR_0621; -.
DR   GCRDb; GCR_0742; -.
DR   GCRDb; GCR_0756; -.
DR   MIM; 126450; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR00242; DOPAMINER.
DR   PRINTS; PR00567; DOPAMINED2R.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Alternative splicing; Disease mutation.
FT   DOMAIN        1     37       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     38     60       1 (POTENTIAL).
FT   DOMAIN       61     71       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     72     97       2 (POTENTIAL).
FT   DOMAIN       98    108       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    109    130       3 (POTENTIAL).
FT   DOMAIN      131    151       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    152    174       4 (POTENTIAL).
FT   DOMAIN      175    186       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    187    210       5 (POTENTIAL).
FT   DOMAIN      211    373       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    374    397       6 (POTENTIAL).
FT   DOMAIN      398    405       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    406    429       7 (POTENTIAL).
FT   DOMAIN      430    443       CYTOPLASMIC (POTENTIAL).
FT   SITE        193    193       IMPLICATED IN CATECHOL AGONIST BINDING
FT                                (BY SIMILARITY).
FT   SITE        194    194       IMPLICATED IN RECEPTOR ACTIVATION
FT                                (BY SIMILARITY).
FT   SITE        197    197       IMPLICATED IN RECEPTOR ACTIVATION
FT                                (BY SIMILARITY).
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     17     17       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     23     23       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    107    182       BY SIMILARITY.
FT   VARSPLIC    242    270       MISSING (IN SHORT ISOFORM).
FT   VARIANT     311    311       S -> C (IN SCHIZOPHRENICS).
FT                                /FTId=VAR_003462.
FT   CONFLICT     40     40       L -> R (IN REF. 7).
SQ   SEQUENCE   443 AA;  50619 MW;  9BF8EA36C988A2E2 CRC64;


  Query Match             31.8%;  Score 645;  DB 1;  Length 443;
  Best Local Similarity   39.1%;  Pred. No. 9.6e-30;
  Matches  160;  Conservative   51;  Mismatches  120;  Indels   78;  Gaps   14;

Qy      43 LLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWL 102
           |||  :: || |||::|: |:|||| ||  ||||| ||||:| ||:|  || ||  | |
Db      43 LLIAVIVFGNVLVCMAVSREKALQTTTNYLIVSLAVADLLVATLVMPWVVYLEVV-GEWK 101

Qy     103 LSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYN-RQGGSRRQLLLIGATWL 161
           |   ||  : :|| :|||| ||||||:||: |||:|: || |    || ::|   |:
Db     102 FSRIHCDIFVTLDVMMCTASILNLCAISIDRYTAVAMPMLYNTRYSSKRRVTVMISIVWV 161

Qy     162 LSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQR 221
           ||  :: |:| |||:    |   | : :  :|||||: ||::|  : ||:|   :  |:|
Db     162 LSFTISCPLLFGLNNA---DQNECIIANPAFVVYSSIVSFYVPFIVTLLVYIKIYIVLRR 218

Qy     222 -------WEVARRAKLHGRAP---------------------------------RRP-- 238
                   :|  : | |||                                   ||
Db     219 RRKRVNTKRSSRAFRAHLRAPLKGNCTHPEDMKLCTVIMKSNGSFPVNRRRVEAARRAQE 278

Qy     239 ------SGPGPP-----SPTPPAPR---LPQDPC--GPDCAPPAPGLPPDPCGSNCAPPD 282
                |   ||      || ||:     || ||   |    | :|  |      |    |
Db     279 LEMEMLSSTSPPERTRYSPIPPSHHQLTLP-DPSHHGLHSTPDSPAKPE----KNGHAKD 333

Qy     283 AVRAAAL-PPQTPPQTRRRRRAKITGR-------ERKAMRVLPVVVGAFLLCWTPFFVVH 334
             : | :   || |  : |   |   |        |:|| ::| :|:| |::|| |||: |
Db     334 HPKIAKIFEIQTMPNGKTRTSLKTMSRRKLSQQKEKKATQMLAIVLGVFIICWLPFFITH 393

Qy     335 ITQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKAL 383
           |    |  |::|| | || ||||||||:||:||| || |||  | | |
Db     394 ILNIHCD-CNIPPVLYSAFTWLGYVNSAVNPIIYTTFNIEFRKAFLKIL 441


RESULT  10
D2DR_CERAE
ID   D2DR_CERAE     STANDARD;      PRT;   443 AA.
AC   P52702;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   D(2) DOPAMINE RECEPTOR.
GN   DRD2.
OS   Cercopithecus aethiops (Green monkey) (Grivet).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercopithecus.
OX   NCBI_TaxID=9534;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=95302446; PubMed=7783157;
RA   Thurkauf A., Hutchinson A., Peterson J., Cornfield L., Meade R.,
RA   Houston K., Harris K., Ross P.C., Gerber K., Ramabhadran T.V.;
RT   "2-phenyl-4-(aminomethyl)imidazoles as potential antipsychotic
RT   agents. Synthesis and dopamine D2 receptor binding.";
RL   J. Med. Chem. 38:2251-2255(1995).
CC   -!- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS
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CC       FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
CC       PROTEINS WHICH INHIBIT ADENYLYL CYCLASE.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U18547; AAB60369.1; -.
DR   GCRDb; GCR_1209; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR00242; DOPAMINER.
DR   PRINTS; PR00567; DOPAMINED2R.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family.
FT   DOMAIN        1     37       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      38    60       1 (POTENTIAL).
FT   DOMAIN        61    71       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      72    97       2 (POTENTIAL).
FT   DOMAIN        98    108      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      109   130      3 (POTENTIAL).
FT   DOMAIN        131   151      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      152   174      4 (POTENTIAL).
FT   DOMAIN        175   186      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      187   210      5 (POTENTIAL).
FT   DOMAIN        211   373      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      374   397      6 (POTENTIAL).
FT   DOMAIN        398   405      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      406   429      7 (POTENTIAL).
FT   DOMAIN        430   443      CYTOPLASMIC (POTENTIAL).
FT   SITE          193   193      IMPLICATED IN CATECHOL AGONIST BINDING
FT                                (BY SIMILARITY).
FT   SITE          194   194      IMPLICATED IN RECEPTOR ACTIVATION
FT                                (BY SIMILARITY).
FT   SITE          197   197      IMPLICATED IN RECEPTOR ACTIVATION
FT                                (BY SIMILARITY).
FT   CARBOHYD      5     5        N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      17    17       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      23    23       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID      107   182      BY SIMILARITY.
SQ   SEQUENCE   443 AA;  50590 MW;  34165BE6460B524D CRC64;


  Query Match           31.7%;  Score 644;  DB 1;  Length 443;
  Best Local Similarity 39.0%;  Pred. No. 1.1e-29;
  Matches  159;  Conservative   52;  Mismatches  121;  Indels   76;  Gaps   14;

Qy      43 LLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWL 102
           |||  :: || |||::|: |:|||| ||  ||||| ||||:| ||:|  || ||  | |
Db      43 LLIAVIVFGNVLVCMAVSREKALQTTTNYLIVSLAVADLLVATLVMPWVVYLEVV-GEWK 101

Qy     103 LSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYN-RQGGSRRQLLLIGATWL 161
           |   ||  : :|| :||||| |||||:||: |||:|: || |    ||  ::|   |:
Db     102 FSKIHCDIFVTLDVMMCTASILNLCAISIDRYTAVAMPMLYNTRYSSKRRVTVMIAIVWV 161

Qy     162 LSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQR 221
           ||  :: |:| |||:    |  | : :  :|||||: ||::|  : ||:|   :  |:|
Db     162 LSFTISCPLLFGLNNA---DQNECIIANPAFVVYSSIVSFYVPFIVTLLVYIKIYIVLRR 218

Qy     222 -------WEVARRAKLHGRAP----------------------------------RRP-- 238
                  :|  : | |||                                      ||
Db     219 RRKRVNTKRSSRAFRSHLRAPLKGNCTHPEDMKLCTVIMKSNGSFPVNRRRVEAARRAQE 278

Qy     239 ------SGPGPP-----SPTPPAPR---LPQDPC--GPDCAPPAPGLPPDPCGSNCAPPD 282
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                |   ||     || ||:     || ||   |   | :|   |:  |     |
Db     279 LEMEMLSSTSPPERTRYSPIPPSHHQLTLP-DPSHHGLHSTPDSPA-KPEKNGHAKNHPK 336

Qy     283 AVRAAALPPQTPPQTRRRRRAKITGR-------ERKAMRVLPVVVGAFLLCWTPFFVVHI 335
           :   :  || |  : |   |   |       |:|| ::| :|:| |::|| |||: ||
Db     337 IAKIFEI--QTMPNGKTRTSLKTMSRRKLSQQKEKKATQMLAIVLGVFIICWLPFFITHI 394

Qy     336 TQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKAL 383
           |  |::|| | || ||||||||:|:|:||| || |||  | | |
Db     395 LNIHCD-CNIPPVLYSAFTWLGYVNSAVNPIIYTTFNIEFRKAFLKIL 441


RESULT  11
D2DR_BOVIN
ID   D2DR_BOVIN     STANDARD;      PRT;   444 AA.
AC   P20288;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   D(2) DOPAMINE RECEPTOR.
GN   DRD2.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90136899; PubMed=2137198;
RA   Chio C.L., Hess G.F., Graham R.S., Huff R.M.;
RT   "A second molecular form of D2 dopamine receptor in rat and bovine
RT   caudate nucleus.";
RL   Nature 343:266-269(1990).
CC   -!- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS
CC       FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
CC       PROTEINS WHICH INHIBIT ADENYLYL CYCLASE.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC       SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X51657; CAA35970.1; -.
DR   PIR; S08163; DYBOD2.
DR   GCRDb; GCR_0488; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR00242; DOPAMINER.
DR   PRINTS; PR00567; DOPAMINED2R.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Alternative splicing.
FT   DOMAIN        1     37       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      38    60       1 (POTENTIAL).
FT   DOMAIN        61    71       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      72    97       2 (POTENTIAL).
FT   DOMAIN        98    108      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      109   130      3 (POTENTIAL).
FT   DOMAIN        131   151      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      152   174      4 (POTENTIAL).
FT   DOMAIN        175   186      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      187   210      5 (POTENTIAL).
FT   DOMAIN        211   374      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      375   398      6 (POTENTIAL).
```

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FT   DOMAIN       399    406       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     407    430       7 (POTENTIAL).
FT   DOMAIN       431    444       CYTOPLASMIC (POTENTIAL).
FT   SITE         193    193       IMPLICATED IN CATECHOL AGONIST BINDING
FT                                 (BY SIMILARITY).
FT   SITE         194    194       IMPLICATED IN RECEPTOR ACTIVATION
FT                                 (BY SIMILARITY).
FT   SITE         197    197       IMPLICATED IN RECEPTOR ACTIVATION
FT                                 (BY SIMILARITY).
FT   CARBOHYD       5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      17     17       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      23     23       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID     107    182       BY SIMILARITY.
FT   VARSPLIC     242    270       MISSING (IN SHORT ISOFORM).
SQ   SEQUENCE   444 AA;  50671 MW;  674371976293017C7 CRC64;


  Query Match             31.3%;  Score 636.5;  DB 1;  Length 444;
  Best Local Similarity   38.2%;  Pred. No. 2.9e-29;
  Matches  156;  Conservative   53;  Mismatches  124;  Indels   75;  Gaps   13;

Qy      43 LLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWL 102
           |||  :: || |||::|: |:|||| ||  ||||| ||||:| ||:|  || ||  | |
Db      43 LLIFVIVFGNVLVCMAVSREKALQTTTNYLIVSLAVADLLVATLVMPWVVYLEVV-GEWK 101

Qy     103 LSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYN-RQGGSRRQLLLIGATWL 161
             |   ||  : :|| :||||| ||||||:||: |||:|: || |    ||  ::|   |:
Db     102 FSRIHCDIFVTLDVMMCTASILNLCAISIDRYTAVAMPMLYNTRYSSKRRVTVMIAIVWV 161

Qy     162 LSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQR 221
           ||  :: |:| |||:    |   | : :  :|||||: ||::|  : ||:|   :  |:|
Db     162 LSFTISCPMLFGLNNT---DQNECIIANPAFVVYSSIVSFYVPFIVTLLVYIKIYIVLRR 218

Qy     222 ------------WEVARRAKLHG---------------------------RAPRRP-- 238
                       :   :| | |                             | ||
Db     219 RRKRVNTKRSSRAFRANLKAPLKGNCTHPEDMKLCTVIMKSNGSFPVNRRRVEAARRAQE 278

Qy     239 ------SGPGPP-----SPTPPAPR---LPQDPC--GPDCAPPAPGLPPDPCGSNCAPPD 282
                |   ||     || ||:     || ||   |    | :|  |     :    |
Db     279 LEMEMLSSTSPPERTRYSPIPPSHHQLTLP-DPSHHGLHSTPDSPAKPEKNGHAKTVNPK 337

Qy     283 AVRAAALPPQTPPQTRRRRRAKITGR-------ERKAMRVLPVVVGAFLLCWTPFFVVHI 335
             :   :  |: |  : |   |   |       |:|| ::| :|:| |::|| |||: ||
Db     338 IAKIFEI--QSMPNGKTRTSLKTMSRRKLSQQKEKKATQMLAIVLGVFIICWLPFFITHI 395

Qy     336 TQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKAL 383
               |::|| | || ||||||||||:|||:||| || |||  | | |
Db     396 LNIHCD-CNIPPVLYSAFTWLGYVNSAVNPIIYTTFNIEFRKAFLKIL 442


RESULT  12
D2DR_MOUSE
ID   D2DR_MOUSE     STANDARD;      PRT;   444 AA.
AC   P13953;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   D(2) DOPAMINE RECEPTOR.
GN   DRD2.
OS   Mus musculus (Mouse), and
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090, 10116;
RN   [1]
RP   SEQUENCE OF 1-241 AND 271-444 FROM N.A.
RC   SPECIES=Rat; TISSUE=Brain;
RX   MEDLINE=89082643; PubMed=2974511;
RA   Bunzow J.R., van Tol H.H.M., Grandy D.K., Albert P., Salon J.,
RA   Christie M., Machida C.A., Neve K.A., Civelli O.;
RT   "Cloning and expression of a rat D2 dopamine receptor cDNA.";
RL   Nature 336:783-787(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Rat;
RX   MEDLINE=90081866; PubMed=2531846;
RA   Eidne K.A., Taylor P.L., Zabavnik J., Saunders P.T.K., Inglis J.D.;
RT   "D2 receptor, a missing exon.";
RL   Nature 342:865-865(1989).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Rat;
RX   MEDLINE=90081872; PubMed=2531847;
RA   Giros B., Sokoloff P., Martres M.-P., Riou J.-F., Emorine L.J.,
RA   Schwartz J.-C.;
RT   "Alternative splicing directs the expression of two D2 dopamine
RT   receptor isoforms.";
RL   Nature 342:923-926(1989).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Rat;
RX   MEDLINE=90081873; PubMed=2480527;
RA   Monsma F.J. Jr., McVittie L.D., Gerfen C.R., Mahan L.C., Sibley D.R.;
RT   "Multiple D2 dopamine receptors produced by alternative RNA
RT   splicing.";
RL   Nature 342:926-929(1989).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Rat;
RX   MEDLINE=90235966; PubMed=2139615;
RA   Rao D.D., McKelvy J., Kebabian J., MacKenzie R.G.;
RT   "Two forms of the rat D2 dopamine receptor as revealed by the
RT   polymerase chain reaction.";
RL   FEBS Lett. 263:18-22(1990).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Rat; STRAIN=SPRAGUE-DAWLEY;
RA   Taylor P.L., Inglis J.D., Eidne K.A.;
RL   Submitted (OCT-1990) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE OF 242-270 FROM N.A.
RC   SPECIES=Rat;
RX   MEDLINE=90147685; PubMed=2137336;
RA   Miller J.C., Wang Y., Filer D.;
RT   "Identification by sequence analysis of a second rat brain cDNA
RT   encoding the dopamine (D2) receptor.";
RL   Biochem. Biophys. Res. Commun. 166:109-112(1990).
RN   [8]
RP   SEQUENCE OF 242-270 FROM N.A.
RC   SPECIES=Rat;
RX   MEDLINE=90201380; PubMed=2138567;
RA   O'Dowd B.F., Nguyen T., Tirpak A., Jarvie K.R., Israel Y., Seeman P.,
RA   Niznik H.B.;
RT   "Cloning of two additional catecholamine receptors from rat brain.";
RL   FEBS Lett. 262:8-12(1990).
RN   [9]
RP   SEQUENCE FROM N.A. (ISOFORM A).
RC   SPECIES=Mouse;
RX   MEDLINE=91122293; PubMed=1991517;
RA   Montmayeur J.P., Bausero P., Amlaiky N., Maroteaux L., Hen R.,
RA   Borrelli E.;
RT   "Differential expression of the mouse D2 dopamine receptor isoforms.";
RL   FEBS Lett. 278:239-243(1991).
RN   [10]
RP   MUTAGENESIS OF SER-193; SER-194; SER-197 AND SER-420.
RC   SPECIES=Rat;
RX   MEDLINE=92333328; PubMed=1321233;
RA   Cox B.A., Henningsen R.A., Spanoyannis A., Neve R.L., Neve K.A.;
RT   "Contributions of conserved serine residues to the interactions of
RT   ligands with dopamine D2 receptors.";
RL   J. Neurochem. 59:627-635(1992).
RN   [11]
RP   INTERACTION WITH NEURABIN II.
RX   MEDLINE=99321921; PubMed=10391935;
RA   Smith F.D., Oxford G.S., Milgram S.L.;
RT   "Association of the D2 dopamine receptor third cytoplasmic loop with
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RT   spinophilin, a protein phosphatase-1-interacting protein.";
RL   J. Biol. Chem. 274:19894-19900(1999).
RN   [12]
RP   3D-STRUCTURE MODELING.
RX   MEDLINE=93038566; PubMed=1358063;
RA   Livingstone C.D., Strange P.G., Naylor L.H.;
RT   "Molecular modelling of D2-like dopamine receptors.";
RL   Biochem. J. 287:277-282(1992).
CC   -!- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS
CC       FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
CC       PROTEINS WHICH INHIBIT ADENYLYL CYCLASE.
CC   -!- SUBUNIT: INTERACTS WITH NEURABIN II.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC       SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X53278; CAA37373.1; -.
DR   EMBL; M32241; AAA41074.1; -.
DR   EMBL; M36831; AAA41075.1; -.
DR   EMBL; X56065; CAA39543.1; -.
DR   EMBL; X55674; CAA39209.1; -.
DR   PIR; S08146; S08146.
DR   PIR; S13921; DYMSD2.
DR   PIR; S21548; S21548.
DR   GCRDb; GCR_0095; -.
DR   GCRDb; GCR_0133; -.
DR   GCRDb; GCR_0135; -.
DR   GCRDb; GCR_0415; -.
DR   GCRDb; GCR_1468; -.
DR   MGD; MGI:94924; Drd2.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR00242; DOPAMINER.
DR   PRINTS; PR00567; DOPAMINED2R.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Alternative splicing.
FT   DOMAIN       1     37       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     38    60       1 (POTENTIAL).
FT   DOMAIN       61    71       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     72    97       2 (POTENTIAL).
FT   DOMAIN       98    108      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     109   130      3 (POTENTIAL).
FT   DOMAIN       131   151      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     152   174      4 (POTENTIAL).
FT   DOMAIN       175   186      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     187   210      5 (POTENTIAL).
FT   DOMAIN       211   374      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     375   398      6 (POTENTIAL).
FT   DOMAIN       399   406      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     407   430      7 (POTENTIAL).
FT   DOMAIN       431   444      CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       211   374      INTERACTS WITH NEURABIN II.
FT   SITE         193   193      IMPLICATED IN CATECHOL AGONIST BINDING.
FT   SITE         194   194      IMPLICATED IN RECEPTOR ACTIVATION.
FT   SITE         197   197      IMPLICATED IN RECEPTOR ACTIVATION.
FT   CARBOHYD      5     5       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     17    17       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     23    23       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID     107   182      BY SIMILARITY.
FT   VARSPLIC     242   270      MISSING (IN SHORT ISOFORM).
FT   MUTAGEN      193   193      S->A: MODERATE DECREASE IN LIGAND
FT                               BINDING. 200-FOLD REDUCTION OF AGONIST-
FT                               MEDIATED CYCLIC AMP INHIBITION.
FT   MUTAGEN      194   194      S->A: SMALL DECREASE IN AGONIST BINDING.
FT                               COMPLETE LOSS OF AGONIST-MEDIATED CYCLIC
FT                               AMP INHIBITION.
FT   MUTAGEN      197   197      S->A: SMALL DECREASE IN AGONIST BINDING.
FT                               18-FOLD REDUCTION OF AGONIST-MEDIATED
FT                               CYCLIC AMP INHIBITION.
FT   MUTAGEN      420   420      S->A: MODERATE DECREASE IN LIGAND
FT                               BINDING.
FT   CONFLICT      99    99      E -> D (IN REF. 5).
FT   CONFLICT     173   173      G -> R (IN REF. 5).
FT   CONFLICT     180   180      N -> G (IN REF. 5).
SQ   SEQUENCE   444 AA;  50903 MW;  216E56CEE5CA32FB CRC64;

  Query Match             31.1%;  Score 631.5;  DB 1;  Length 444;
  Best Local Similarity   38.2%;  Pred. No. 5.5e-29;
  Matches  156;  Conservative   51;  Mismatches  126;  Indels   75;  Gaps   13;

Qy      43 LLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWL 102
           |||  :: || |||::|: |:|||| ||  ||||| ||||:| ||:|  || ||  | |
Db      43 LLIFIIVFGNVLVCMAVSREKALQTTTNYLIVSLAVADLLVATLVMPWVVYLEVV-GEWK 101

Qy     103 LSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYN-RQGGSRRQLLLIGATWL 161
           |   ||  : :|| :|||| |||||:||: |||:|: || |   || ::|   |:
Db     102 FSRIHCDIFVTLDVMMCTASILNLCAISIDRYTAVAMPMLYNTRYSSKRRVTVMIAIVWV 161

Qy     162 LSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWA------- 214
           ||  :: |:| |||:    |   | : :  :|||||: ||::|  : ||:|
Db     162 LSFTISCPLLFGLNNT---DQNECIIANPAFVVYSSIVSFYVPFIVTLLVYIKIYIVLRK 218

Qy     215 ------TFRGLQRWEVARRAKLHGR---------------------------APRRP-- 238
                 | |  : :    :  | |                            | ||
Db     219 RRKRVNTKRSSRAFRANLKTPLKGNCTHPEDMKLCTVIMKSNGSFPVNRRRMDAARRAQE 278

Qy     239 ------SGPGPP-----SPTPPAPR---LPQDPC--GPDCAPPAPGLPPDPCGSNCAPPD 282
                 |   ||      || ||:     || ||   |   | :|  |      :    |
Db     279 LEMEMLSSTSPPERTRYSPIPPSHHQLTLP-DPSHHGLHSNPDSPAKPEKNGHAKIVNPR 337

Qy     283 AVRAAALPPQTPPQTRRRRRAKITGR-------ERKAMRVLPVVVGAFLLCWTPFFVVHI 335
           :   :  || |  : |   |  |        |:|| ::| :|:| |::|| ||| : ||
Db     338 IAKFFEI--QTMPNGKTRTSLKTMSRRKLSQQKEKKATQMLAIVLGVFIICWLPFFITHI 395

Qy     336 TQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKAL 383
             |  |::|| | || |||||||||:||:||| || |||  | | |
Db     396 LNIHCD-CNIPPVLYSAFTWLGYVNSAVNPIIYTTFNIEFRKAFMKIL 442


RESULT  13
D2D1_XENLA
ID   D2D1_XENLA     STANDARD;      PRT;   442 AA.
AC   P24628;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   D(2) DOPAMINE RECEPTOR 1.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=91200321; PubMed=1826663;
RA   Martens G.J.M., Molhuizen H.O.F., Groeneveld D., Roubos E.W.;
RT   "Cloning and sequence analysis of brain cDNA encoding a Xenopus D2
RT   dopamine receptor.";
RL   FEBS Lett. 281:85-89(1991).
CC   -!- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS
CC       FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
CC       PROTEINS WHICH INHIBITS ADENYLYL CYCLASE. IN XENOPUS D2R IS
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CC       INVOLVED IN THE REGULATION OF THE MELANOTROPE CELLS OF THE
CC       INTERMEDIATE PITUITARY DURING BACKGROUND ADAPTATION OF THE ANIMAL.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- TISSUE SPECIFICITY: BRAIN; PITUITARY.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X59500; CAA42088.1; -.
DR   PIR; S14827; DYXLD2.
DR   GCRDb; GCR_0256; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR00242; DOPAMINER.
DR   PRINTS; PR00567; DOPAMINED2R.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family.
FT   DOMAIN       1     31       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    32     54       1 (POTENTIAL).
FT   DOMAIN      55     65       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    66     91       2 (POTENTIAL).
FT   DOMAIN      92    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   103    124       3 (POTENTIAL).
FT   DOMAIN     125    145       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   146    168       4 (POTENTIAL).
FT   DOMAIN     169    180       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   181    204       5 (POTENTIAL).
FT   DOMAIN     205    372       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   373    396       6 (POTENTIAL).
FT   DOMAIN     397    404       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   405    428       7 (POTENTIAL).
FT   DOMAIN     429    442       CYTOPLASMIC (POTENTIAL).
FT   SITE       187    187       IMPLICATED IN CATECHOL AGONIST BINDING
FT                               (BY SIMILARITY).
FT   SITE       188    188       IMPLICATED IN RECEPTOR ACTIVATION
FT                               (BY SIMILARITY).
FT   SITE       191    191       IMPLICATED IN RECEPTOR ACTIVATION
FT                               (BY SIMILARITY).
FT   CARBOHYD     5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    15     15       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    18     18       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID   101    176       BY SIMILARITY.
SQ   SEQUENCE   442 AA;  49738 MW;  95AD1B779680C6BB CRC64;


  Query Match             31.0%;  Score 629.5;  DB 1;  Length 442;
  Best Local Similarity   36.4%;  Pred. No. 7e-29;
  Matches  151;  Conservative   59;  Mismatches  120;  Indels   85;  Gaps   12;

Qy      43 LLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWL 102
           ||:  :: || |||::|: |:|||| ||  |||||| ||||:| ||:|  || ||  | |
Db      37 LLVFVIVFGNVLVCIAVSREKALQTTTNYLIVSLAVADLLVATLVMPWAVYMEVV-GEWR 95

Qy     103 LSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYN-RQGGSRRQLLLIGATWL 161
             |   ||  : :|| :|||||  |||||:||: |||:|: || |    ||  ::|   |:
Db      96 FSRIHCDIFVTLDVMMCTASILNLCAISIDRYTAVAMPMLYNTRYSSKRRVTVMISVVWV 155

Qy     162 LSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQR 221
           || |:: |:| |||:   :   || :::  :|:|||: ||::|  : ||:|      :|
Db     156 LSFAISCPLLFGLNNTGSK---VCIIDNPAFVIYSSIVSFYVPFIVTLLVY------VQI 206

Qy     222 WEVARR-----------------------------------AKLHGRAPR--------RP 238
           : | |:                                   | :|  |         :
Db     207 YIVLRKRRKRVNTKRNSRGVAVDAHKDKCTHPEDVKLCSVFVKSNGSFPADKKKVILVQE 266

Qy     239 SGPGPP-------SPTPPAPRLPQDPCGPD---CAPPA-----------PGLPPDPCGS 276
           :|  |        | | |  :        ||    | ||           |   |
Db     267 AGKHPEDMEMEMMSSTSPPEKTKHKSASPDHNQLAVPATSNQCKNASLTSPVESPYKAEK 326

Qy     277 NCAPPDAVR-AAALPPQTPPQTRRRRRAKITG-------RERKAMRVLPVVVGAFLLCWT 328
           |  | |: : |     |: |  : |   |          :|:|| ::| :|:| |::||
Db     327 NGHPKDSTKPAKVFEIQSMPNGKTRTSIKTMSKKKLSQHKEKKATQMLAIVLGVFIICWL 386

Qy     329 PFFVVHITQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKAL 383
           |||::||    |  |::|  | || ||||||||||:||:||| || |||  | | |
Db     387 PFFIIHILNMHC-NCNIPQALYSAFTWLGYVNSAVNPIIYTTFNVEFRKAFIKIL 440


RESULT  14
D2DR_MELGA
ID   D2DR_MELGA     STANDARD;      PRT;   436 AA.
AC   O73810;
DT   20-AUG-2001 (Rel. 40, Created)
DT   20-AUG-2001 (Rel. 40, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   D(2) DOPAMINE RECEPTOR.
GN   DRD2.
OS   Meleagris gallopavo (Common turkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX   NCBI_TaxID=9103;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NICHOLAS LARGE WHITE; TISSUE=Brain;
RA   Schnell S.A., You S., Foster D.N., el Halawani M.E.;
RT   "Molecular cloning and tissue distribution of an avian D2 dopamine
RT   receptor from the domestic turkey (Meleagris gallopavo).";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: THIS IS ONE OF THE FIVE TYPES (D1 TO D5) OF RECEPTORS
CC       FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
CC       PROTEINS WHICH INHIBIT ADENYLYL CYCLASE (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF056201; AAD03818.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR00242; DOPAMINER.
DR   PRINTS; PR00567; DOPAMINED2R.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family.
FT   DOMAIN       1     34       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    35     57       1 (POTENTIAL).
FT   DOMAIN      58     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    69     94       2 (POTENTIAL).
FT   DOMAIN      95    105       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   106    127       3 (POTENTIAL).
FT   DOMAIN     128    148       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   149    171       4 (POTENTIAL).
FT   DOMAIN     172    183       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   184    207       5 (POTENTIAL).
FT   DOMAIN     208    366       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   367    390       6 (POTENTIAL).
FT   DOMAIN     391    398       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   399    422       7 (POTENTIAL).
FT   DOMAIN     423    436       CYTOPLASMIC (POTENTIAL).
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FT   DISULFID    104    179       BY SIMILARITY.
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     15     15       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     21     21       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   436 AA;  49389 MW;  5FB13F684532C53B CRC64;


  Query Match             30.3%;  Score 615;  DB 1;  Length 436;
  Best Local Similarity   37.4%;  Pred. No. 4.5e-28;
  Matches  154;  Conservative   52;  Mismatches  118;  Indels   88;  Gaps   13;

Qy      43 LLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWL 102
           |||  :: || |||::|: |:|||| ||  ||||| ||||:| ||:|  || ||  | |
Db      40 LLIFVIVFGNVLVCMAVSREKALQTTTNYLIVSLAVADLLVATLVMPWVVYLEVV-GEWR 98

Qy     103 LSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYN-RQGGSRRQLLLIGATWL 161
           |   ||  : :|| :|||| ||||||:||: | |:|: || |    ||  ::|   |:
Db      99 FSRIHCDIFVTLDVMMCTASILNLCAISIDRYTAAAMPMLYNTRYSSKRRVTVMIACVWV 158

Qy     162 LSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQR 221
           || |:::|:| |||    |:   | : :  :|||||| ||::|  : ||:|   :  |:
Db     159 LSFAISSPILFGLNKADERE---CIIANPAFVVYSSVVSFYVPFIVTLLVYVQIYMVLR- 214

Qy     222 WEVARRAKLHGRAPRRPSGPGPPSPTPPAPRLPQDPCG---------------------- 259
               || | |     : |  |  | |  ||   :| |
Db     215 ----RRRKRH----TKRSSHGLDSDT-HAPL--KDKCTHPENVKLGTVIVKSNGSFQVNK 263

Qy     260 ----------------PDCAPP--------APG-----LPPDPCGSNCAPPDAVR----- 285
                           :||        ||      :|     |    |  |
Db     264 RKCEAESHIKMEMEMMSSTSPPERTIVKAAAPSNHQLVVPVASSRSTLDSPGKVEKNGHA 323

Qy     286 ------AAALPPQTPPQTRRR--------RRAKITGRERKAMRVLPVVVGAFLLCWTPFF 331
                 |     |: |  : |         ||     :|:|| ::| :|:| |::|| |||
Db     324 KENLHTAKVFEIQSMPNGKTRSTLLKAMNRRKLSQQKEKKATQMLAIVLGVFIICWLPFF 383

Qy     332 VVHITQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKAL 383
           : ||    |  |::|| : || |||||||||:||:||| || |||  | | |
Db     384 ITHILNMHCD-CNIPPAMYSAFTWLGYVNSAVNPIIYTTFNIEFRKAFMKIL 434


RESULT  15
A2AA_PIG
ID   A2AA_PIG       STANDARD;      PRT;   450 AA.
AC   P18871;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR).
GN   ADRA2A OR A2AR.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 212-232.
RC   TISSUE=Liver;
RX   MEDLINE=91009167; PubMed=2170371;
RA   Guyer C.A., Horstman D.A., Wilson A.L., Clark J.D., Kragoe E.J. Jr.,
RA   Limbird L.E.;
RT   "Cloning, sequencing, and expression of the gene encoding the porcine
RT   alpha 2-adrenergic receptor. Allosteric modulation by Na+, H+, and
RT   amiloride analogs.";
RL   J. Biol. Chem. 265:17307-17317(1990).
RN   [2]
RP   MUTAGENESIS OF CYS 442.
RX   MEDLINE=93216775; PubMed=8385131;
RA   Kennedy M.E., Limbird L.E.;
RT   "Mutations of the alpha 2A-adrenergic receptor that eliminate
RT   detectable palmitoylation do not perturb receptor-G-protein
RT   coupling.";
RL   J. Biol. Chem. 268:8003-8011(1993).
CC   -!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC       INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC       PROTEINS.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: ALPHA2-ADRENERGIC RECEPTOR SHOWS AN ALLOSTERIC
CC       MODULATION BY NA+, H+, AND AMILORIDE ANALOGS.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J05652; AAA30984.1; -.
DR   PIR; A38316; A38316.
DR   HSSP; P29274; 1MMH.
DR   GCRDb; GCR_0101; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR00558; ADRENRGCA2AR.
DR   PRINTS; PR01103; ADRENERGICR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT   DOMAIN        1     33       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     34     59       1 (POTENTIAL).
FT   DOMAIN       60     70       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     71     96       2 (POTENTIAL).
FT   DOMAIN       97    106       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    107    129       3 (POTENTIAL).
FT   DOMAIN      130    149       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    150    173       4 (POTENTIAL).
FT   DOMAIN      174    192       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    193    217       5 (POTENTIAL).
FT   DOMAIN      218    374       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    375    399       6 (POTENTIAL).
FT   DOMAIN      400    409       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    410    430       7 (POTENTIAL).
FT   DOMAIN      431    450       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     10     10       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     14     14       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    106    188       BY SIMILARITY.
FT   LIPID       442    442       PALMITATE.
FT   SITE        113    113       IMPLICATED IN LIGAND BINDING (BY
FT                                SIMILARITY).
FT   SITE        200    200       IMPLICATED IN CATECHOL AGONIST BINDING
FT                                (BY SIMILARITY).
FT   SITE        204    204       IMPLICATED IN CATECHOL AGONIST BINDING
FT                                (BY SIMILARITY).
FT   MUTAGEN     442    442       C->A,S: LOSS OF PALMITOYLATION.
SQ   SEQUENCE   450 AA;  48975 MW;  79D7D5B47372074E CRC64;


  Query Match             28.6%;  Score 581;  DB 1;  Length 450;
  Best Local Similarity   34.1%;  Pred. No. 3.6e-26;
  Matches  152;  Conservative   62;  Mismatches  142;  Indels   90;  Gaps   13;

Qy      18 PAAGASAGASAGLAGQGAAA-----------LVGGVLLIGAVLAGNSLVCVSVATERAL 65
           | || ::       | || |             : |:|::  |  || || ::| | |||
Db       6 PEAGNASWNGTEAPGGGARATPYSLQVTLTLVCLAGLLMLFTVF-GNVLVIIAVFTSRAL 64

Qy      66 QTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCTASIFN 125
           : | |:||||:||:|:| ||:|  : :||  | |      |:  :|:||  ||:|| :
Db      65 KAPQNLFLVSLASADILVATLVIPFSLANEVM-GYWYFGKAWCEIYLALDVLFCTSSIVH 123

Qy     126 LCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVR---GRDP 182
           |||||:||: ::   : || :   ||   :|   |::|| :: | |  :       |: |
Db     124 LCAISLDRYWSITQAIEYNLKRTPRRIKAIIVTVWVISAVISFPPLISIEKKAGGGGQQP 183

Qy     183 AVCRLEDRD---YVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARR----------- 227
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          |  | |  |   ||: | : ||| || :|:|:|      :: :::|:|
Db    184 AEPRCEINDQKWYVISSCIGSFFAPCLIMILVY------VRIYQIAKRRTRVPPSRRGPD 237

Qy    228 --AKLHGRAPRRPSGPGPP------------------SPTPPAPRLPQDPCGPDCAPPA 266
            | | | | |||:| ||                    :|  |||  |:|  | |    :
Db    238 AAAALPGGAERRPNGLGPERGVGRVGAEAEPLPVQLNGAPGEPAPAGPRDADGLDLEESS 297

Qy    267 PG----LPPDPCGSNCAPPDAVRAAA--------LP-----------PQTPPQTRRRRRA 303
                || |  |   |    :| |        ||           | |     |   |
Db    298 SSEHAERPPGPRRSERGPRAKSKARASQVKPGDSLPRRGPGAPGPGAPATGAGEERGGVA 357

Qy    304 KIT------GRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLG 357
          | :       ||::   || ||:| |::|| |||  :   |:   ||||| |     | |
Db    358 KASRWRGRQNREKRFTFVLAVVIGVFVVCWFPFFFTYTLTAV--GCSVPPTLFKFFFWFG 415

Qy    358 YVNSALNPVIYTVFNAEFRNVFRKAL 383
          | ||:|||||||:|| :|}  |:| |
Db    416 YCNSSLNPVIYTIFNHDFRRAFKKIL 441


Search completed: February 13, 2002, 17:42:34
Job time: 200 sec
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: February 13, 2002, 17:38:59 ; Search time 25.44 Seconds
(without alignments)
2225.133 Million cell updates/sec

Title: US-09-550-103-1
Perfect score: 2031
Sequence: 1 MGNRSTADADGLLAGRGPAA.....YTVFNAEFRNVFRKALRACC 387

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1034	50.9	374	13	O42322	O42322 cyprinus ca
2	774	38.1	278	13	O42321	O42321 cyprinus ca
3	658.5	32.4	399	4	Q13167	Q13167 homo sapien
4	658.5	32.4	514	13	Q9PSA6	Q9psa6 fugu rubrip
5	645	31.8	443	4	Q9UPA9	Q9upa9 homo sapien
6	644	31.7	445	4	Q9NZR3	Q9nzr3 homo sapien
7	638	31.4	511	13	Q9PSA7	Q9psa7 fugu rubrip
8	637.5	31.4	414	6	Q9GK99	Q9gk99 canis famil
9	635.5	31.3	414	6	Q9GKA0	Q9gka0 canis famil
10	624	30.7	443	6	Q9GJU1	Q9gju1 canis famil
11	623.5	30.7	374	13	O42320	O42320 cyprinus ca
12	577	28.4	447	4	Q9BZK0	Q9bzk0 homo sapien
13	574.5	28.3	399	5	Q9NG02	Q9ng02 apis mellif
14	567	27.9	419	5	O77254	O77254 boophilus m
15	566	27.9	462	4	Q9HB49	Q9hb49 homo sapien
16	557	27.4	450	4	Q9BZK1	Q9bzk1 homo sapien
17	527	25.9	419	4	Q9P2Q5	Q9p2q5 homo sapien
18	527	25.9	419	6	Q9N2E1	Q9n2e1 gorilla gor
19	527	25.9	422	6	Q9N297	Q9n297 gorilla gor
20	526	25.9	419	6	Q9N2E2	Q9n2e2 pan troglod
21	526	25.9	419	6	Q9N2E0	Q9n2e0 pongo pygma
22	526	25.9	422	6	Q9N298	Q9n298 pan troglod
23	526	25.9	422	6	Q9N296	Q9n296 pongo pygma
24	521	25.7	408	13	Q98998	Q98998 xenopus lae
25	516	25.4	394	5	Q9NHF3	Q9nhf3 aplysia cal
26	515.5	25.4	407	6	Q9MZ00	Q9mz00 sus scrofa
27	503	24.8	394	5	Q9NJS6	Q9njs6 aplysia kur
28	495.5	24.4	477	5	Q9BMA9	Q9bma9 mamestra br
29	489	24.1	603	5	Q9VG57	Q9vg57 drosophila
30	487	24.0	402	5	O44198	O44198 apis mellif
31	486.5	24.0	405	6	Q9GJS6	Q9gjs6 ovis aries
32	485.5	23.9	405	6	Q9GL57	Q9gl57 ovis aries
33	485.5	23.9	405	6	Q9GJT0	Q9gjt0 ovis aries
34	484.5	23.9	405	6	Q9GL56	Q9gl56 ovis aries
35	484	23.8	383	6	Q9GL28	Q9gl28 bradypus tr
36	484	23.8	508	5	Q9VCZ3	Q9vcz3 drosophila
37	483	23.8	389	6	Q9GL07	Q9gl07 phoca vitul
38	482.5	23.8	559	11	Q9QW71	Q9qw71 rattus sp.
39	482.5	23.8	571	6	Q9TTM9	Q9ttm9 sus scrofa
40	481	23.7	391	6	Q9GL06	Q9gl06 sus scrofa
41	480	23.6	383	6	Q9GL20	Q9gl20 cynopterus
42	476.5	23.5	385	5	Q24038	Q24038 drosophila
43	474	23.3	885	5	O61232	O61232 lymnaea sta
44	473	23.3	393	6	Q9GL16	Q9gl16 hippopotamu
45	473	23.3	393	6	Q9GL15	Q9gl15 macrotus ca

ALIGNMENTS

RESULT 1
O42322
ID O42322 PRELIMINARY; PRT; 374 AA.
AC O42322;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE D4B DOPAMINE RECEPTOR.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=RETINA;
RA Hirano J., Archer S.N., Djamgoz M.B.A.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; Y14633; CAA74977.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR002106; AA_tRNA_ligase_II.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 374 AA; 42004 MW; 8DE52E86BE88A717 CRC64;

Query Match 50.9%; Score 1034; DB 13; Length 374;
Best Local Similarity 54.6%; Pred. No. 1.8e-65;
Matches 214; Conservative 43; Mismatches 89; Indels 46; Gaps 6;

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Qy      22 ASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADL 81
           |:  ||:         ||: |:|||  :: || |||:|| ||:||:| || |||||| |||
Db       3 ANLTASSHSTNYNFPALIFGILLIVIIICGNVLVCLSVYTEKALKTTTNYFIVSLAVADL 62

Qy      82 LLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPL 141
           |||:||||||||:| | | | |:  ||| || ||| ||||||||||||:|||:||::||
Db      63 LLAVLVLPLFVYAEFQDGVWSLNMTLCDGLMTMDVMLCTASIFNLCAISIDRFIAVSIPL 122

Qy     142 RYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSF 201
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Db    123 NYNRKHVGQRQIVLLSATWILASAVASPVMFGINNVPNRDHSECKLEDNNYVVYSSVCSF 182

Qy    202 FLPCPLMLLLYWATFRGLQRWEVARRAKL----------HGRAPRRPSGPGPPSPTPPA 250

Db    183 FVPCPIMLLLYCGMFRGLRNWEEARKAKLRSSMQACRKLQEAAASLQPLS-GLPPPLPPV 241

Qy    251 ----------PRLPQDPCGPD--CAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTR 298

Db    242 IKKDLTDITLEELEQDPDSPEPVCMLAYPG------------------GTYHEHRNQNR 282

Qy    299 RRRRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGY 358

Db    283 QRKRAKINGRERKAMRVLPVVVGAFLFCWTPFFVVHTMRALCEDCYIPSSVTSIVTWLGY 342

Qy    359 VNSALNPVIYTVFNAEFRNVFRK---ALRACC 387

Db    343 VNSALNPVIYTVFNTEFRKFFRKFLPTLPNCC 374


RESULT   2
O42321
ID   O42321      PRELIMINARY;      PRT;   278 AA.
AC   O42321;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   D4A DOPAMINE RECEPTOR.
OS   Cyprinus carpio (Common carp).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
OX   NCBI_TaxID=7962;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=RETINA;
RA   Hirano J., Archer S.N., Djamgoz M.B.A.;
RL   Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Y14630; CAA74974.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR002106; AA_tRNA_ligase_II.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SQ   SEQUENCE   278 AA;  31516 MW;  717C6207BFC58977 CRC64;


  Query Match             38.1%;  Score 774;  DB 13;  Length 278;
  Best Local Similarity   53.2%;  Pred. No. 2.9e-47;
  Matches  159;  Conservative   30;  Mismatches   64;  Indels   46;  Gaps    7;

Qy    114 MDVALCTASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCG 173

Db      1 MDVMLCTASIFNLCAISIDRFIAVSIPLNYNRKHVDQRQIVLLSATWILALAVASPVMFG 60

Qy    174 LNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKL--- 230

Db     61 INNVPNRDHSECKLEDNNYVVYSSVCSFFVPCPIMLMLYCGMFRGLRNWEEARKAKLRSS 120

Qy    231 --------HGRAPRRPSGPGPPSPTPPA----------PRLPQDPCGPDCAPPAP-GLPP 271

Db    121 MQACRKLQEAAASLQPLS-GLPPPLPPVIEKDLSDITLEELDHDHY-PDPDSPGPVSMLT 178

Qy    272 DPCGSNCAPPDAVRAAALPPQTPPQTRRRRRAKITGRERKAMRVLPVVVGAFLLCWTPFF 331

Db    179 HPVGG------------------QNRRRKRAKINGRERKAMRVLPVVVGVFLFCWTPFF 219

Qy    332 VVHITQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRK---ALRACC 387

Db    220 VVHTLRALCEDCYIPSSVTSIVTWLGYVNSALNPIIYTVFNTEFRKFFRKFLPTLPNCC 278
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RESULT   3
Q13167
ID   Q13167      PRELIMINARY;      PRT;   399 AA.
AC   Q13167;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   DOPAMINE D3 RECEPTOR.
GN   DRD3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RX   MEDLINE=96233802; PubMed=8678117;
RA   Griffon N., Crocq M.A., Pilon C., Martres M.P., Mayerova A.,
RA   Uyanik G., Burgert E., Duval F., Macher J.P., Javoy-Agid F.,
RA   Tamminga C.A., Schwartz J.C., Sokoloff P.;
RT   "Dopamine D3 receptor gene: organization, transcript variants, and
RT   polymorphism associated with schizophrenia.";
RL   Am. J. Med. Genet. 67:63-70(1996).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; U25441; AAB08750.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
SQ   SEQUENCE   399 AA;  44111 MW;  C9F7F4F456F4533A CRC64;


  Query Match             32.4%;  Score 658.5;  DB 4;  Length 399;
  Best Local Similarity   38.1%;  Pred. No. 5.6e-39;
  Matches  152;  Conservative   53;  Mismatches  141;  Indels   53;  Gaps    9;

Qy     21 GASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAAD 80

Db     16 GAENSTGASQARPHAYYALSYCALILAIVFGNGLLCMAVLKERALQTTTNYLVVSLAVAD 75

Qy     81 LLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVP 140

Db     76 LLVATLVMPWVVYLEVTGGVWNFS-ICCDVFVTLDVMMCTASILNLCAISIDRYTAVVMP 134

Qy    141 LRYNR---QGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSS 197

Db    135 VHYQHGTGQSSCRRVALMITAVWVLAFAVSCPLLFGFNTT--GNPTVCSISNPDFVIYSS 192

Qy    198 VCSFFLPCPLMLLLY---WATFRGLQRWEVARRAKLHGRAPRRPSGPGPPSPTPPAPRLP 254

Db    193 VVSFYLPFGVTVLVYARIYVVLKQRRRKRILTRQNSQCNSVR-------------PGFP 238

Qy    255 QDPCGPD------------CAPPAPGLPP-DPCGSNCAPPDAVRAAALP---PQTPPQTR 298

Db    239 QQTLSPDPAHLELKRYYSICQDTALGGPGFQERGGELKREEKTRNSLSPTIAPKLSLEVR 298

Qy    299 RRRRAKITG--------------RERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACS 344

Db    299 KLSNGRLSTSLKLGPLQPRGVPLREKKATQMVAIVLGTFIVCWLPFFLTHVLNTHCQTCH 358

Qy    345 VPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKAL 383

Db    359 VSPELYSATTWLGYVNSALNPVIYTTFNIEFRKAFLKIL 397


RESULT   4
Q9PSA6
ID   Q9PSA6      PRELIMINARY;      PRT;   514 AA.
AC   Q9PSA6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
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DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   D3-TYPE DOPAMINE RECEPTOR HOMOLOG.
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95309911; PubMed=7789977;
RA   Macrae A.D., Brenner S.;
RT   "Analysis of the dopamine receptor family in the compact genome of the
RT   puffer fish Fugu rubripes.";
RL   Genomics 25:436-446(1995).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
SQ   SEQUENCE   514 AA;  57849 MW;  0B80B395F1AE2123 CRC64;


  Query Match             32.4%;  Score 658.5;  DB 13;  Length 514;
  Best Local Similarity   34.7%;  Pred. No. 7.1e-39;
  Matches  167;  Conservative   52;  Mismatches  111;  Indels  151;  Gaps   13;

Qy      43 LLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWL 102
           ||| |:: || |||::|  ||:||| ||  :|||| ||||:| ||:|  || || |||||
Db      43 LLILAIVFGNVLVCLAVLRERSLQTTTNYLVVSLAVADLLVASLVMPWAVYLEVVGGAWL 102

Qy     103 LSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQL-LLIGATWL 161
           |   |:  : :|| :||||| ||||||:||: || :|: ||    ||::: ::|   |:
Db     103 FSRLYCNIFVTLDVMMCTASILNLCAISIDRYTAVVMPVLYNTTHRSRKRVFVMIAIVWV 162

Qy     162 LSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQR 221
           |: ||: |:| | |     || || : : |:|:|||| ||:||  : ||:|   :  |:
Db     163 LAFAVSCPLLFGFNTT--DDPMVCSISNPDFVIYSSVVSFYLPFIITLLVYIRIYIFLR- 219

Qy     222 WEVARRAKLHGRAPRRPSGPGPPSPTPPA--------PRLPQD---------------PC 258
           || ::   |  :|||   |   ||:         |:  ||                  |
Db     220 ---MRRKRI---AFGQPSGKVQPGSAPPSAETCLQETPQAKQDLSPIRIKVQSVELPGPS 273

Qy     259 GPDCAP-------PAPG------LPPDPCGSNCA-------------------------- 279
           |           |  |       |||    : |:
Db     274 KPSLLSGCLWRKRPKTGPVENSMLPPVDTQNCCSISHASCGRTELDLEQERGEEGEEVAE 333

Qy     280 ------PPDAVRAA-------------ALPP---------------------------- 291
                ||  || :              :| |
Db     334 GSQREQPP--VRMSCEVKDLSNGRTHTSLHPAYHSHTLNTRFRTMHAREKKATQMLAIVL 391

Qy     292 ----QTPP-------------------------QTRRRRRAKITGRERKAMRVLPVVVGA 322
           : ||                             |   |   :  ||:|| ::| :|:|
Db     392 GSQREQPPVRMSCEVKDLSNGRTHTSLHPAYHSHTLNTRFRTMHAREKKATQMLAIVLGV 451

Qy     323 FLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKA 382
           ||:|| |||| ||    |  | :|| | || ||||||||||||||| || |||  | |
Db     452 FLICWLPFFVTHILNTHCRTCYIPPGLYSAFTWLGYVNSALNPVIYTTFNIEFRRAFIKI 511

Qy     383 L 383
           |
Db     512 L 512


RESULT   5
Q9UPA9
ID   Q9UPA9      PRELIMINARY;      PRT;   443 AA.
AC   Q9UPA9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   DOPAMINE D2 RECEPTOR.
GN   DRD2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PARTIAL SEQUENCE FROM N.A.
RX   MEDLINE=91365356; PubMed=1679742;
RA   Hauge X.Y., Grandy D.K., Eubanks J.H., Evans G.A., Civelli O.,
RA   Litt M.;
RT   "Detection and characterization of additional DNA polymorphisms in the
RT   dopamine D2 receptor gene.";
RL   Genomics 10:527-530(1991).
RN   [2]
RP   PARTIAL SEQUENCE FROM N.A.
RX   MEDLINE=96065034; PubMed=8533775;
RA   Castiglione C.M., Deinard A.S., Speed W.C., Sirugo G., Rosenbaum H.C.,
RA   Zhang Y., Grandy D.K., Grigorenko E.L., Bonne-Tamir B., Pakstis A.J.,
RA   Kidd J.R., Kidd K.K.;
RT   "Evolution of haplotypes at the DRD2 locus.";
RL   Am. J. Hum. Genet. 57:1445-1456(1995).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98431008; PubMed=9760208;
RA   Kidd K.K., Morar B., Castiglione C.M., Zhao H., Pakstis A.J.,
RA   Bonne-Tamir B., Lu R.-B., Goldman D., Lee C., Suk Nam Y., Grandy D.K.,
RA   Jenkins T., Kidd J.R.;
RT   "A global survey of haplotype frequencies and linkage disequilibrium
RT   at the DRD2 locus.";
RL   Hum. Genet. 103:211-227(1998).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Kidd K.K.;
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF050737; AAC78779.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ   SEQUENCE   443 AA;  50628 MW;  24B31576C544AE22 CRC64;


  Query Match             31.8%;  Score 645;  DB 4;  Length 443;
  Best Local Similarity   39.1%;  Pred. No. 5.5e-38;
  Matches  160;  Conservative   51;  Mismatches  120;  Indels   78;  Gaps   14;

Qy      43 LLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWL 102
           |||  :: || |||::|: |:|||| ||  ||||| ||||:| ||:|  || ||  | |
Db      43 LLIAVIVFGNVLVCMAVSREKALQTTTNYLIVSLAVADLLVATLVMPWVVYLEVV-GEWK 101

Qy     103 LSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYN-RQGGSRRQLLLIGATWL 161
           |   ||  : :|| :||||| ||||||:||: |||:|: || |    ||  ::|   |:
Db     102 FSRIHCDIFVTLDVMMCTASILNLCAISIDRYTAVAMPMLYNTRYSSKRRVTVMISIVWV 161

Qy     162 LSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQR 221
           ||  :: |:| |||:    |   | : :  :|||||: ||::|  : ||:|   :  |:|
Db     162 LSFTISCPLLFGLNNA---DQNECIIANPAFVVYSSIVSFYVPFIVTLLVYIKIYIVLRR 218

Qy     222 -------WEVARRAKLHGRAP-----------------------------------RRP-- 238
                  :|  : | |||                                     ||
Db     219 RRKRVNTKRSSRAFRAHLRAPLKGNCTHPEDMKLCTVIMKSNGSFPVNRRRVEAARRAQE 278

Qy     239 ------SGPGPP-----SPTPPAPR---LPQDPC--GPDCAPPAPGLPPDPCGSNCAPPD 282
                |   ||      || ||:     || ||   |    | :|  |      |    |
Db     279 LEMEMLSSTSPPERTRYSPIPPSHHQLTLP-DPSHHGLHSTPDSPAKPE----KNGHAKD 333
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Qy     283 AVRAAAL-PPQTPPQTRRRRRAKITGR-------ERKAMRVLPVVVGAFLLCWTPFFVVH 334
Db     334 HPKIAKIFEIQTMPNGKXRTSLKTMSRRKLSQQKEKKATQMLAIVLGVFIICWLPFFITH 393

Qy     335 ITQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKAL 383
Db     394 ILNIHCD-CNIPPVLYSAFTWLGYVNSAVNPIIYTTFNIEFRKAFLKIL 441


RESULT   6
Q9NZR3
ID   Q9NZR3      PRELIMINARY;      PRT;   445 AA.
AC   Q9NZR3;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   DOPAMINE RECEPTOR D2LONGER.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN STRIATUM;
RX   MEDLINE=20185651; PubMed=10719223;
RA   Seeman P., Nam D., Ulpian C., Liu I.S.C., Tallerico T.;
RT   "New dopamine receptor, D2(Longer), with unique TG splice site, in
RT   human brain.";
RL   Brain Res. Mol. Brain Res. 76:132-141(2000).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF176812; AAF61479.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ   SEQUENCE   445 AA;  50846 MW;  111674E96E087FD6 CRC64;


  Query Match             31.7%;  Score 644;  DB 4;  Length 445;
  Best Local Similarity   38.9%;  Pred. No. 6.5e-38;
  Matches  160;  Conservative   51;  Mismatches  120;  Indels   80;  Gaps   14;

Qy      43 LLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWL 102
Db      43 LLIAVIVFGNVLVCMAVSREKALQTTTNYLIVSLAVADLLVATLVMPWVVYLEVV-GEWK 101

Qy     103 LSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYN-RQGGSRRQLLLIGATWL 161
Db     102 FSRIHCDIFVTLDVMMCTASILNLCAISIDRYTAVAMPMLYNTRYSSKRRVTVMISIVWV 161

Qy     162 LSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQR 221
Db     162 LSFTISCPLLFGLNNA---DQNECIIANPAFVVYSSIVSFYVPFIVTLLVYIKIYIVLRR 218

Qy     222 -------WEVARRAKLHGRAP----------------------------------RRP 238
Db     219 RRKRVNTKRSSRAFRAHLRAPLKGNCTHPEDMKLCTVIMKSNGSFPVNRRRVVQEAARRA 278

Qy     239 --------SGPGPP-----SPTPPAPR---LPQDPC--GPDCAPPAPGLPPDPCGSNCAP 280
Db     279 QELEMEMLSSTSPPERTRYSPIPPSHHQLTLP-DPSHHGLHSTPDSPAKPE----KNGHA 333

Qy     281 PDAVRAAAL-PPQTPPQTRRRRRAKITGR-------ERKAMRVLPVVVGAFLLCWTPFFV 332
Db     334 KDHPKIAKIFEIQTMPNGKTRTSLKTMSRRKLSQQKEKKATQMLAIVLGVFIICWLPFFI 393

Qy     333 VHITQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKAL 383
Db     394 THILNIHCD-CNIPPVLYSAFTWLGYVNSAVNPIIYTTFNIEFRKAFLKIL 443


RESULT   7
Q9PSA7
ID   Q9PSA7      PRELIMINARY;      PRT;   511 AA.
AC   Q9PSA7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   D2-TYPE DOPAMINE RECEPTOR HOMOLOG.
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95309911; PubMed=7789977;
RA   Macrae A.D., Brenner S.;
RT   "Analysis of the dopamine receptor family in the compact genome of the
RT   puffer fish Fugu rubripes.";
RL   Genomics 25:436-446(1995).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
SQ   SEQUENCE   511 AA;  57333 MW;  615DAC74D8C9A08E CRC64;


  Query Match             31.4%;  Score 638;  DB 13;  Length 511;
  Best Local Similarity   32.6%;  Pred. No. 2e-37;
  Matches  155;  Conservative   62;  Mismatches  118;  Indels  140;  Gaps   10;

Qy      43 LLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWL 102
Db      41 LLIFVIVFGNVLVCMAVSREKALQTTTNYLIVSLAVADLLVATLVMPWVVYLEVV-GEWR 99

Qy     103 LSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQL-LLIGATWL 161
Db     100 FSKIHCDIFVTLDVMMCTASILNLCAISIDRYTAVAMPMLYNTRYSSRRRVTVMISVVWV 159

Qy     162 LSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQR 221
Db     160 LSFAISCPLLFGLNNTATRDQSLCFIANPAFVVYSSIVSFYVPFIVTLLVYVQIYVVLRK 219

Qy     222 WEVARRAKLHGRAPRR-PSGPGPPSPT------------------------------ 247
Db     220 ----RRKRVNTKPKQRLCQAADPDIPTSLKDKCTHPEDVRLCTMIVKSNGSFPVNKKKVI 275

Qy     248 --------------------------PPAPRLP----------------QDPCGPDCAP 264
Db     276 FIKDGVNEVEGLELDELNYCGGSHKQPPPQQQPRALGDTPATSHQLLMSTKANASPTSTP 335

Qy     265 PAP----------GLPPDPCGSNCAPPDAVR--------------------------A 286
Db     336 PTPPEEGQRTEKNGDPTKEAQGNPAPVVALRNGKTQTSLKTLSKRKISQQKEKKATQMLA 395

Qy     287 AALP-----------------PQTPPQTRRRRRAKITGRERKAMRVLPVVVGAFLLCWT 328
Db     396 IVLPTKEAQGNPAPVVALRNGKTQTSLKTLSKRKIS-QQKEKKATQMLAIVLGVFIICWL 454

Qy     329 PFFVVHITQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKAL 383
Db     455 PFFITHILNTHCTRCKVPAEMYNAFTWLGYVNSAVNPIIYTTFNVEFRKAFIKIL 509


RESULT   8
Q9GK99
ID   Q9GK99      PRELIMINARY;      PRT;   414 AA.
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AC   Q9GK99;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   DOPAMINE D2 RECEPTOR SHORT ISOFORM.
GN   DRD2.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20510028; PubMed=11054572;
RA   Myeong H., Jeoung D., Kim H., Ha J.H., Lee Y., Kim K.H., Park C.,
RA   Kaang B.;
RT   "Genomic analysis and functional expression of canine dopamine D2
RT   receptor.";
RL   Gene 257:99-107(2000).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF293964; AAG34497.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ   SEQUENCE   414 AA;  47288 MW;  4E330ADCA00FCB5C CRC64;

  Query Match             31.4%;  Score 637.5;  DB 6;  Length 414;
  Best Local Similarity   37.8%;  Pred. No. 1.7e-37;
  Matches  148;  Conservative   58;  Mismatches  113;  Indels   73;  Gaps    9;

Qy      43 LLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWL 102
           |||  :: || |||::|: |:|||| ||  ||||| |||| :| ||:|  || ||  | |
Db      43 LLIFIIVFGNVLVCMAVSREKALQTTTNYLIVSLAVADLLVATLVMPWVVYLEVV-GEWK 101

Qy     103 LSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYN-RQGGSRRQLLLIGATWL 161
             |   ||  : :|| :||||| ||||||:||: |||:|: || |    ||  ::|   |:
Db     102 FSRIHCDIFVTLDVMMCTASILNLCAISIDRYTAVAMPMLYNTRYSSKRRVTVMIAIVWV 161

Qy     162 LSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQR 221
           ||  :: |:| |||:    |   | : :  :|||||: ||::|  : ||:|   :  |:|
Db     162 LSFTISCPLLFGLNNT---DQNECIIANPAFVVYSSIVSFYVPFIVTLLVYIKIYIVLRR 218

Qy     222 WEVARRAKLHGRAPRRPSGPGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPP 281
             || ::: :   |       :|   | |  |:                |  :   |: :||
Db     219 ----RRKRVNTKRSSRAFRANLKAPLKEAARRAQE-----------LEMEML-SSTSPP 261

Qy     282 DAVRAAALPP-----------------------------------------QTPPQTR 298
           :  | : :||                                        |: |  :
Db     262 ERTRYSPIPPSHHQLTLPDPSHHGLHSTADSPAKPEKNGHAKDHPKIAKIFEIQSMPNGK 321

Qy     299 RRRRAKITGR-------ERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVS 351
           |   |   |       |:|| ::| :|:| |::|| |||: ||    |  |::|| | |
Db     322 TRTSLKTMSRRKLSQQKEKKATQMLAIVLGVFIICWLPFFITHILNIHC-ECNIPPVLYS 380

Qy     352 AVTWLGYVNSALNPVIYTVFNAEFRNVFRKAL 383
           | |||||||||:||:||| || |||  | | |
Db     381 AFTWLGYVNSAVNPIIYTTFNIEFRKAFLKIL 412


RESULT   9
Q9GKA0
ID   Q9GKA0      PRELIMINARY;      PRT;   414 AA.
AC   Q9GKA0;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   DOPAMINE D2 RECEPTOR SHORT ISOFORM.
GN   DRD2.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20510028; PubMed=11054572;
RA   Myeong H., Jeoung D., Kim H., Ha J.H., Lee Y., Kim K.H., Park C.,
RA   Kaang B.;
RT   "Genomic analysis and functional expression of canine dopamine D2
RT   receptor.";
RL   Gene 257:99-107(2000).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF293962; AAG34495.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ   SEQUENCE   414 AA;  47289 MW;  7DAD2AD48621CD74 CRC64;

  Query Match             31.3%;  Score 635.5;  DB 6;  Length 414;
  Best Local Similarity   41.0%;  Pred. No. 2.4e-37;
  Matches  157;  Conservative   48;  Mismatches  123;  Indels   55;  Gaps   12;

Qy      43 LLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWL 102
           |||  :: || |||::|: |:|||| ||  ||||| |||+:| ||:|  || ||  | |
Db      43 LLIFIIVFGNVLVCMAVSREKALQTTTNYLIVSLAVADLLVATLVMPWVVYLEVV-GEWK 101

Qy     103 LSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYN-RQGGSRRQLLLIGATWL 161
             |   ||  : :|| :||||| ||||||:||: |||:|: || |    ||  ::|   |:
Db     102 FSRIHCDIFVTLDVMMCTASILNLCAISIDRYTAVAMPMLYNTRYSSKRRVTVMIAIVWV 161

Qy     162 LSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGL-- 219
           ||  :: |:| |||:    |   | : :  :|||||: ||::|  : ||:|   :  |
Db     162 LSFTISCPLLFGLNNT---DQNECIIANPAFVVYSSIVSFYVPFIVTLLVYIKIYIVLRR 218

Qy     220 -------QRWEVARRAKLHG---RAPRRP--------SGPGPP-----SPTPPAPR---L 253
                  :|   | || |      | ||          |   ||     || ||:     |
Db     219 RRKRVNTERSSRAFRANLKAPLKEAARRAQELEMEMLSSTSPPERTRYSPIPPSHHQLTL 278

Qy     254 PQDPCGPDCAPPAPGL------PPDPCGSNCAPPDAVRAAALPPQTPPQTRRRRRAKITG 307
           |          |   ||      |  |  :  |       |     |: |  : |   |
Db     279 PD--------PSHHGLHSTADSPAKPEKNGHAKDHPKIAKIFEIQSMPNGKTRTSLKTMS 330

Qy     308 R-------ERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360
           |       |:|| ::| :|:| |::|| |||: ||    |  |::|| | || |||||||
Db     331 RRKLSQQKEKKATQMLAIVLGVFIICWLPFFITHILNIHC-ECNIPPVLYSAFTWLGYVN 389

Qy     361 SALNPVIYTVFNAEFRNVFRKAL 383
           ||:||:||| || |||  | | |
Db     390 SAVNPIIYTTFNIEFRKAFLKIL 412


RESULT  10
Q9GJU1
ID   Q9GJU1      PRELIMINARY;      PRT;   443 AA.
AC   Q9GJU1;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   DOPAMINE D2 RECEPTOR.
GN   DRD2.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20510028; PubMed=11054572;
RA   Myeong H., Jeoung D., Kim H., Ha J.H., Lee Y., Kim K.H., Park C.,
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RA   Kaang B.;
RT   "Genomic analysis and functional expression of canine dopamine D2
RT   receptor.";
RL   Gene 257:99-107(2000).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF293963; AAG34496.1; -.
DR   EMBL; AF293962; AAG34494.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ   SEQUENCE   443 AA;  50562 MW;  50B7A17B6645DC3C CRC64;


  Query Match             30.7%;  Score 624;  DB 6;  Length 443;
  Best Local Similarity   37.9%;  Pred. No. 1.7e-36;
  Matches  156;  Conservative   50;  Mismatches  122;  Indels   84;  Gaps   12;

Qy      43 LLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWL 102
           |||  :: || |||::|: |:|||| ||  ||||| ||||:| ||:|  || ||  | |
Db      43 LLIFIIVFGNVLVCMAVSREKALQTTTNYLIVSLAVADLLVATLVMPWVVYLEVV-GEWK 101

Qy     103 LSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYN-RQGGSRRQLLLIGATWL 161
           |   ||  : :|| :|||||  ||||||:||: |||:|: || |    ||  ::|   |:
Db     102 FSRIHCDIFVTLDVMMCTASILNLCAISIDRYTAVAMPMLYNTRYSSKRRVTVMIAIVWV 161

Qy     162 LSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQR 221
           ||  :: |:| |||:    |   | : :  :|||||: ||::|  : ||:|   :  |:|
Db     162 LSFTISCPLLFGLNNT---DQNECIIANPAFVVYSSIVSFYVPFIVTLLVYIKIYIVLRR 218

Qy     222 ----------WEVARRAKLHG--------------------------RAPRRP-- 238
                    :   :| | |                            | ||
Db     219 RRKRVNTERSSRAFRANLKAPLKGNCTHPEDMKLCTVIMKSNGSFPVNRRRVEAARRAQE 278

Qy     239 ------SGPGPP-----SPTPPAPR---LPQDPCGPDCAPPAPGL------PPDPCGSNC 278
                |   ||     || ||:     ||         |   ||      |  |  :
Db     279 LEMEMLSSTSPPERTRYSPIPPSHHQLTLPD--------PSHHGLHSTADSPAKPEKNGH 330

Qy     279 APPDAVRAAALPPQTPPQTRRRRRAKITGR-------ERKAMRVLPVVVGAFLLCWTPFF 331
           |      |      |: |  : |   |   |       |:|| ::| :|:| |::|| |||
Db     331 AKDHPKIAKIFEIQSMPNGKTRTSLKTMSRRKLSQQKEKKATQMLAIVLGVFIICWLPFF 390

Qy     332 VVHITQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKAL 383
           : ||    |  |::|| | || |||||||||:||:||| || |||  | | |
Db     391 ITHILNIHC-ECNIPPVLYSAFTWLGYVNSAVNPIIYTTFNIEFRKAFLKIL 441


RESULT  11
O42320
ID   O42320      PRELIMINARY;      PRT;   374 AA.
AC   O42320;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   D2 DOPAMINE RECEPTOR (FRAGMENT).
OS   Cyprinus carpio (Common carp).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
OX   NCBI_TaxID=7962;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=RETINA;
RA   Hirano J., Archer S.N., Djamgoz M.B.A.;
RL   Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; Y14632; CAA74976.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
FT   NON_TER       1      1
SQ   SEQUENCE   374 AA;  42107 MW;  2B39DA9965303480 CRC64;


  Query Match             30.7%;  Score 623.5;  DB 13;  Length 374;
  Best Local Similarity   40.1%;  Pred. No. 1.5e-36;
  Matches  154;  Conservative   43;  Mismatches  108;  Indels   79;  Gaps   11;

Qy      59 VATERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVAL 118
           |: |:|||| ||  ||||| :|||||  ||:|  || ||  | |  |   || |: :|| :
Db       1 VSREKALQTTTNYLIVSLAVSDLLLATLVMPWAVYLEVV-GEWRFSRIHCDILLTLDVMM 59

Qy     119 CTASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQL-LLIGATWLLSAAVAAPVLCGLNDV 177
           ||||| ||| ||:||: |||:|| || :  |||:: |:| | | || |:: |:| |||:
Db      60 CTASILNLCVISIDRYTAVAMPLLYNTRYSSRRRVALMIAAVWFLSFAISCPLLFGLNNT 119

Qy     178 RGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGR--AP 235
             ::   |   | :|||||| ||::|  : ||:|      :|   | ||    ||  ||
Db     120 ASQEGRDCSFADPAFVVYSSVASFYVPFIVTLLVY------VQICVVLRR---RGRRTAP 170

Qy     236 RRPSGPGPP-------------------------SPTPPAPR-------------LPQD 256
           |  |  |                           | | ||:                |  :
Db     171 SRRHGLHPEPRDAQRSRKNKCTHPEDVKLCTLIVKPPPAAPQHKRVMLVKEAVVHPLDVE 230

Qy     257 P---CGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRRRRAKITGR----- 308
           |     ||       : | |       |   || |   |    ||   | : | |
Db     231 PVCFLSPDRGQQQQLVAPSPA---LLGPGPRRATA---QENTHTRHGWRDRNTDREKGAA 284

Qy     309 -------------ERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTW 355
                       |||| ::| :|:| |::|| ||||: |: :| | :| : | | |||||
Db     285 AKERARGRLSQQKERKATQMLAIVLGVFIICWLPFFMTHVLKAHCGSCCISPSLYSAVTW 344

Qy     356 LGYVNSALNPVIYTVFNAEFRNVF 379
           |||:|||:|||||| || |||  |
Db     345 LGYLNSAVNPVIYTTFNIEFRQAF 368


RESULT  12
Q9BZK0
ID   Q9BZK0      PRELIMINARY;      PRT;   447 AA.
AC   Q9BZK0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ALPHA 2B ADRENERGIC RECEPTOR.
GN   ADRA2B.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=11056163;
RA   Small K.M., Brown K.M., Forbes S.L., Liggett S.B.;
RT   "Polymorphic Deletion of Three Intracellular Acidic Residues of the
RT   alpha 2B-Adrenergic Receptor Decreases G Protein-coupled Receptor
RT   Kinase-mediated Phosphorylation and Desensitization.";
RL   J. Biol. Chem. 276:4917-4922(2001).
DR   EMBL; AF316895; AAK01635.1; -.
KW   Receptor.
FT   VARIANT     298    300       EEE -> KRR.
SQ   SEQUENCE   447 AA;  49566 MW;  B33D4B5B719C1C45 CRC64;


  Query Match             28.4%;  Score 577;  DB 4;  Length 447;
  Best Local Similarity   33.6%;  Pred. No. 3.4e-33;
  Matches  148;  Conservative   66;  Mismatches  125;  Indels  102;  Gaps   15;

Qy      33 QGAAALVGGV-LLIGAVLAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLF 91
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Db     10 QATAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADILVATLIIPFS 69

Qy     92 VYSEVQGGAWLLSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYNRQGGSRR 151
          : :|:  | |      |:  :|:||  ||:|| :|||||:||: ||:  | || :   ||
Db     70 LANELL-GYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPRR 128

Qy    152 QLLLIGATWLLSAAVAAPVLCGLND----VRGRDPAVCRL-EDRDYVVYSSVCSFFLPCP 206
           :|   ||:|| :: | |    |     |||    |:| ::  |:: ||: ||| ||
Db    129 IKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQ--CKLNQEAWYILASSIGSFFAPCL 186

Qy    207 LMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSGPGPPSPTPPAP---------RLP--- 254
          :|:|:|      |: : :|:|:  : | ||   |||      | |          :||
Db    187 IMILVY------LRIYLIAKRS--NRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALA 238

Qy    255 ----------------------QDPCGPDCAPPAPGLPPDP--------CGSN------ 277
                               :  |    ||:    |:         |::
Db    239 SVASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAE 298

Qy    278 --------CAP---PDAVRAAALPPQTPPQTRR----------------------RRRA 303
                | |   | :  :|  ||   ||  |                      ||||
Db    299 EEEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRA 358

Qy    304 KITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPA-CSVPPRLVSAVTWLGYVNSA 362
          ::| ||::   || ||:| |:||| |||  :   |:||  | ||  |     |:|| ||:
Db    359 QLT-REKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPKHCKVPHGLFQFFFWIGYCNSS 417

Qy    363 LNPVIYTVFNAEFRNVFRKAL 383
          |||||||:|| :||  ||: |
Db    418 LNPVIYTIFNQDFRRAFRRIL 438


RESULT  13
Q9NG02
ID   Q9NG02      PRELIMINARY;      PRT;   399 AA.
AC   Q9NG02;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   G-PROTEIN COUPLED RECEPTOR.
GN   TYR1.
OS   Apis mellifera (Honeybee).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC   Apoidea; Apidae; Apis.
OX   NCBI_TaxID=7460;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Blenau W., Balfanz S., Baumann A.;
RT   "Amtyr1: characterization of a gene from honeybee (Apis mellifera)
RT   brain encoding a functional tyramine receptor.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AJ245824; CAB76374.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ   SEQUENCE   399 AA;  44650 MW;  F5FE4E4F13336433 CRC64;


  Query Match           28.3%;  Score 574.5;  DB 5;  Length 399;
  Best Local Similarity   37.6%;  Pred. No. 4.6e-33;
  Matches  150;  Conservative   66;  Mismatches  158;  Indels   25;  Gaps   13;

Qy      2 GNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVAT 61
          |   | | |  : | ||      |::  :    ||:|  | |::  || ||:|| :|| |
Db      8 GGTMTEDYD--MTGCGPPE-EETGSNLPVWEAAAASLTLGFLVLATVL-GNALVILSVFT 63

Qy     62 ERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCTA 121
```

```
          | |:   | |||||| ||| :|:||:| |  : :  | |:    ||   :  ||  |||
Db     64 YRPLRIVQNFFIVSLAVADLAVAILVMP-FNVAYLLLGKWIFGIHLCKLWLTCDVLCCTA 122

Qy    122 SIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLND-VRGR 180
          || ||||::||: |:  |: | ::   :| |  |   |:|| |:::| | | ||
Db    123 SILNLCAIALDRYWAITDPINYAQKRTLKRVLATIAGVWILSGAISSPPLAGWNDWPEEL 182

Qy    181 DPAV-CRLEDRD-YVVYSSVCSFFLPCPLMLL----LYWATFRGLQRWEVARRAKLHG-- 232
          :|   |:|  |  ||:|||: |||:|  || |    :| || | |:  | ||:::::
Db    183 EPGTPCQLTRRQGYVIYSSLGSFFIPLLLMSLVYLEIYLATRRRLR--ERARQSRINAVQ 240

Qy    233 RAPRRPSGPGPPSPTP-------PAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVR 285
          |  | :.    | :          ||    |  | |    :      |:     : |
Db    241 STRHREADDAEESVSSETNHNERSTPRSHAKPSLIDDEPTEVTIGGGGTTSSRRTTGS-R 299

Qy    286 AAALPPQTPPQTRRRRRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSV 345
          |||           |:|  :: :|||:| | | |::| |::|| |||::::    || |
Db    300 AAATTTTVYQFIEERQRISLS-KERRAARTLGVIMGVFVVCWLPFFLMYVIVPFCPDCCP 358

Qy    346 PPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKALR 384
            |:|  :|||||||||||||:|||:||.::|  ||: ||
Db    359 SDRMVYFITWLGYVNSALNPLIYTIFNLDYRRAFRRLLR 397


RESULT  14
O77254
ID   O77254      PRELIMINARY;      PRT;   419 AA.
AC   O77254;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   G-PROTEIN COUPLED RECEPTOR.
OS   Boophilus microplus (Cattle tick).
OC   Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC   Parasitiformes; Ixodida; Ixodidae; Boophilus.
OX   NCBI_TaxID=6941;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=N-STRAIN; TISSUE=WHOLE LARVAE;
RA   Baxter G.D., Barker S.C.;
RT   "Isolation of an octopamine-like, G-protein coupled receptor cDNA from
RT   the cattle tick, Boophilus microplus.";
RL   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AJ010743; CAA09335.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
SQ   SEQUENCE   419 AA;  47090 MW;  8DEDCAE2E50F3FA5 CRC64;


  Query Match           27.9%;  Score 567;  DB 5;  Length 419;
  Best Local Similarity   38.9%;  Pred. No. 1.6e-32;
  Matches  142;  Conservative   52;  Mismatches  139;  Indels   32;  Gaps   11;

Qy     39 VGGVLLIGAV----LAGNSLVCVSVATERALQTPTNSFIVSLAAADLLLALLVLPLFVYS 94
          ||  | :  :    : || ||  ||   | |:|  | |:|||| ||: :||||:|  |
Db     58 VGTALSLSFITVFTVVGNVLVICSVFNHRPLRTVQNVFLVSLALADIAVALLVMPFNVAY 117

Qy     95 EVQGGAWLLSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLL 154
          :  | |:     |:  :  ||  ||||| ||||::||: |:  |: | ::   || ||
Db    118 SIM-GRWVFGLHFCELWLTCDVLCCTASILNLCAIALDRYWAIHDPINYAQKRTLRRVLL 176

Qy    155 LIGATWLLSAAVAAPVLCGLND--VRGRDPAVCRL-EDRDYVVYSSVCSFFLPCPLMLLL 211
            |   |::|| :: | | | ||   :  :   ||| ::  ||:||:  |||:|  :| ::
Db    177 SIFLVWVISALISVPPLIGWNDWPEQFDETTPCRLTQETGYVLYSASGSFFIPLLIMSIV 236

Qy    212 YWATFRGLQRWEVARRAKLHGRAPRRPSGPGPPSPTPPAPRLPQDPC-----GPDCAPPA 266
          |   |       :| | :|  ||    :   | | |  |  :           |  :
```

```
Db    237 YLKIF-------LATRRRLRERA--NAAAKVPSSATRCAATVEHSVALLQERHPSSSEET 287

Qy    267 PGLPPDPCGSNC--APPDAVRAAAL-----PPQTPPQTRRRRRAKIT-GRERKAMRVLPV 318
          |  ||   |      |  |   :  |     ||     |    | :|:  |||:| ||| :
Db    288 P--PPQHRGQTTENRPSLADTSVTLEQNGRPPSVKVFTCWEERQRISLSRERRAARVLGI 345

Qy    319 VVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNV 378
          |:| |:||| |||:::::| | |  |    |||: :|||||||||||||||||||| :||
Db    346 VMGVFVLCWLPFFIMYVTAAFCDHCVQSDRLVNFITWLGYVNSALNPVIYTVFNTDFRRA 405

Qy    379 FRKAL 383
          ||  |
Db    406 FRSLL 410


RESULT  15
Q9HB49
ID   Q9HB49      PRELIMINARY;      PRT;   462 AA.
AC   Q9HB49;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ALPHA 2C ADRENERGIC RECEPTOR.
GN   ADRA2C.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20390061; PubMed=10801795;
RA   Small K.M., Forbes S.L., Rahman F.F., Bridges K.M., Liggett S.B.;
RT   "A four amino acid deletion polymorphism in the third intracellular
RT   loop of the human alpha 2C-adrenergic receptor confers impaired
RT   coupling to multiple effectors.";
RL   J. Biol. Chem. 275:23059-23064(2000).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF280399; AAG28076.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT   VARIANT     239    239       L -> R.
FT   VARIANT     329    329       E -> Q.
FT   VARIANT     401    401       S -> I.
FT   VARIANT     446    446       R -> P.
SQ   SEQUENCE   462 AA;  49522 MW;  E1EF9CA21E7F6EDA CRC64;


  Query Match             27.9%;  Score 566;  DB 4;  Length 462;
  Best Local Similarity   34.4%;  Pred. No. 2.1e-32;
  Matches  157;  Conservative   50;  Mismatches  144;  Indels  106;  Gaps   14;

Qy      2 GNRSTADADGLLAGRGPAAGA-SAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
            |:   |:| |  |  ||  |  |||| |||     ||:||   ||   : || || ::|
Db     27 GSGGVANASG--ASWGPPRGQYSAGAVAGL-----AAVVG--FLIVFTVVGNVLVVIAVL 77

Qy     61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
          | |||: | | |:||||:||:|:| ||:|  : :|:    |      |   :|:||  ||
Db     78 TSRALRAPQNLFLVSLASADILVATLVMPFSLANELM-AYWYFGQVWCGVYLALDVLFCT 136

Qy    121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVL--------- 171
          :|| :|||||:||: :|   : || :   ||    | | ||:|| :: | |
Db    137 SSIVHLCAISLDRYWSVTQAVEYNLKRTPRRVKATIVAVWLISAVISFPPLVSLYRQPDG 196

Qy    172 -----CGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVAR 226
               |||||            :  |:: | : ||| || :| |:|           : |
Db    197 AAYPQCGLND------------ETWYILSSCIGSFFAPCLIMGLVY---------ARIYR 235

Qy    227 RAKLHGRA---PRRPSGPGPPSPTPPAPRLPQDPCGPD--CAPPAPGLPPDPCGSNC--- 278
          |||  |     | | ||   |||           | :  ||||   : ||   :
Db    236 VAKLRTRTLSEKRAPVGPDGASPTTENGLGAAAGAGENGHCAPPPADVEPDESSAAAERR 295

Qy    279 --------------------------APPDAVRAAALPPQTPP---------------- 295
                                       | | |  : || :  |
Db    296 RRRGALRRGGRRRAGAEGGAGGADGQGAGPGAAESGALTASRSPGPGGRLSRASSRSVEF 355

Qy    296 --QTRRRRRAKI------TGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALC-PACSVP 346
               ||| |: :        ||::   || ||:| |:||| ||| :    :|  || ||
Db    356 FLSRRRRARSSVCRRKVAQAREKRFTFVLAVVMGVFVLCWFPFFFSYSLYGICREACQVP 415

Qy    347 PRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKAL 383
            |     |:|| ||:|||||||||| :||  |:  |
Db    416 GPLFKFFFWIGYCNSSLNPVIYTVFNQDFRRSFKHIL 452


Search completed: February 13, 2002, 17:42:14
Job time: 195 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: February 13, 2002, 17:36:54 ; Search time 25.16 Seconds
(without alignments)
1139.363 Million cell updates/sec

Title: US-09-550-103-1
Perfect score: 2031
Sequence: 1 MGNRSTADADGLLAGRGPAA.....YTVFNAEFRNVFRKALRACC 387

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101:*
1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	DB	ID	Description
1	2031	100.0	387	21	AAB12901	Human dopamine D4
2	2028	99.9	387	19	AAW40503	Human dopamine D4
3	2026	99.8	387	16	AAR70734	Human D4 dopamine
4	2026	99.8	387	21	AAB15760	Human D4 receptor
5	2011	99.0	387	15	AAR48948	Sequence encoded b
6	2011	99.0	387	17	AAR96213	Recombinant human
7	2008	98.9	387	13	AAR25335	D4 dopamine recept
8	1993	98.1	387	16	AAR75957	Human dopamine D4
9	1993	98.1	387	18	AAW01749	Human dopamine D4
10	1985	97.7	419	15	AAR48949	Sequence encoded b
11	1985	97.7	419	17	AAR96214	Recombinant human
12	1961	96.6	467	15	AAR48950	Sequence encoded b
13	1961	96.6	467	17	AAR96215	Recombinant human
14	1548.5	76.2	315	15	AAR48707	G-protein coupled
15	1548.5	76.2	315	17	AAW02679	G-protein coupled
16	1471	72.4	385	21	AAB15759	Rat D4 receptor pr
17	683	33.6	446	12	AAR14551	D-3 dopaminergic r
18	683	33.6	446	12	AAR15349	D-3 dopaminergic r
19	679	33.4	400	13	AAR24246	Human D3 dopaminer
20	675	33.2	400	13	AAR24247	Mutant human D3 do
21	659.5	32.5	414	12	AAR11800	Human retinal dopa
22	647	31.9	415	11	AAR05539	Rat D2 dopamine re
23	647	31.9	415	20	AAY01598	Rat D2 dopamine re
24	646	31.8	415	17	AAW09388	Mouse dopamine D2
25	645	31.8	443	11	AAR05541	Human pituitary do
26	645	31.8	443	12	AAR11497	Hman dopamine D2 r
27	645	31.8	443	20	AAY01600	Human pituitary do
28	645	31.8	443	22	AAB69075	Human dopamine rec
29	631.5	31.1	444	12	AAR10544	D2 dopamine recept
30	631.5	31.1	444	17	AAW09387	Mouse dopamine D2
31	629.5	31.0	353	20	AAY13738	Human dopamine D2
32	607	29.9	317	15	AAR48706	G-protein coupled
33	607	29.9	317	17	AAW02678	G-protein coupled
34	577	28.4	447	22	AAE00989	Human alpha2B-adre
35	575.5	28.3	450	22	AAE00990	Human alpha2B-adre
36	564	27.8	458	15	AAR54834	Human derived adre
37	560	27.6	314	15	AAR48705	G-protein coupled
38	560	27.6	314	17	AAW02677	G-protein coupled
39	559.5	27.5	379	18	AAW33185	Corn barnacle G-pr
40	548.5	27.0	487	12	AAR14149	Human alpha 2 beta
41	548.5	27.0	487	18	AAW11804	Human alpha-2b adr
42	537	26.4	330	15	AAR48699	G-protein coupled
43	537	26.4	330	17	AAW02671	G-protein coupled
44	532.5	26.2	476	18	AAW24089	Balanus amphitrite
45	529	26.0	601	13	AAR21931	D.melanogaster oct

ALIGNMENTS

RESULT 1
AAB12901
ID AAB12901 standard; protein; 387 AA.
XX
AC AAB12901;
XX
DT 14-NOV-2000 (first entry)
XX
DE Human dopamine D4 receptor amino acid sequence.
XX
KW Dopamine D4 receptor; human; schizophrenia; depression; diagnosis;
KW methylation.
XX
OS Homo sapiens.
XX
PN US6080549-A.
XX
PD 27-JUN-2000.
XX
PF 08-APR-1997; 97US-0833703.
XX
PR 08-APR-1997; 97US-0833703.
XX
PA (UYNE-) UNIV NORTHEASTERN.
XX
PI Deth RC;
XX
DR WPI; 2000-474787/41.
XX
PT Diagnosing schizophrenia or depression in an individual involves
PT comparing phospholipid methylation levels and D4 receptor levels
PT contributing to modified phospholipid methylation levels, to normal
PT levels -
XX

```
PS   Disclosure; Fig 1; 12pp; English.
XX
CC   The present sequence represents the human dopamine D4 receptor protein
CC   sequence. Dopamine receptors are members of the G-protein coupled
CC   receptor family. It is thought that a defect in the dopamine pathways of
CC   neuronal transmission may be involved in causing schizophrenia, with
CC   particular emphasis on the role of dopamine D4 receptors. The present
CC   invention relates to a method for assisting in the diagnosis of
CC   schizophrenia or depression in an individual and involves correlating
CC   biochemical abnormality in phospholipid methylation to abnormal
CC   modification of the dopamine D4 receptor. Normal modification of the
CC   dopamine D4 receptor occurs at the methionine residue at position 331 of
CC   the human D4 receptor protein sequence. The method is used in the
CC   diagnosis of schizophrenia or depression in an individual.
XX
SQ   Sequence   387 AA;


  Query Match             100.0%;  Score 2031;  DB 21;  Length 387;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-146;
  Matches  387;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mgnrstadadgllagrgpaagasagasaglagqgaaalvggvlligavlagnslvcvsva 60

Qy      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 teralqtptnsfivslaaadlllallvlplfvysevqggawllsprlcdalmamdvalct 120

Qy     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 asifnlcaisvdrfvavavplrynrqggsrrqllligatwllsaavaapvlcglndvrgr 180

Qy     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 dpavcrledrdyvvyssvcsfflpcplmlllywatfrglqrwevarraklhgraprrpsg 240

Qy     241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 pgppsptppaprlpqdpcgpdcappapglppdpcgsncappdavraaalppqtppqtrrr 300

Qy     301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 rrakitgrerkamrvlpvvvgafllcwtpffvvhitqalcpacsvpprlvsavtwlgyvn 360

Qy     361 SALNPVIYTVFNAEFRNVFRKALRACC 387
           |||||||||||||||||||||||||||
Db     361 salnpviytvfnaefrnvfrkalracc 387


RESULT   2
AAW40503
ID   AAW40503 standard; protein; 387 AA.
XX
AC   AAW40503;
XX
DT   14-JUL-1998  (first entry)
XX
DE   Human dopamine D4 receptor protein.
XX
KW   Dopamine receptor; D4 receptor; D4R; therapy; treatment; schizophrenia;
KW   adenosyl group; methionine adenosyl transferase; MAT deficient.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          34..55
FT                   /label= transmembrane_helical_element
FT   Region          74..96
FT                   /label= transmembrane_helical_element
FT   Region          110..131
FT                   /label= transmembrane_helical_element
FT   Region          152..174
FT                   /label= transmembrane_helical_element
FT   Region          192..213
FT                   /label= transmembrane_helical_element
FT   Modified-site   313
FT                   /note= "adenosyl group added"
FT   Region          315..335
FT                   /label= transmembrane_helical_element
FT   Region          351..371
FT                   /label= transmembrane_helical_element
XX
PN   US5738998-A.
XX
PD   14-APR-1998.
XX
PF   24-MAY-1995;   95US-0449651.
XX
PR   24-MAY-1995;   95US-0449651.
XX
PA   (DETH/) DETH R C.
XX
PI   Deth RC;
XX
DR   WPI; 1998-250415/22.
XX
PT   Method for assessing schizophrenia treatments - by measuring
PT   modified dopamine D4 receptor levels
XX
PS   Disclosure; Fig 2; 15pp; English.
XX
CC   This sequence represents the human dopamine D4 receptor which is used in
CC   a novel method for assessing the effectiveness of a therapeutic or
CC   process for treating schizophrenia. The method involves determining the
CC   amount of dopamine D4 receptor (D4R) in a tissue sample which have and
CC   have not been modified by the addition of an adenosyl group on Met313 of
CC   the receptor. D4Rs are usually modified with the enzyme methionine
CC   adenosyl transferase (MAT), which is deficient in sufferers of
CC   schizophrenia, resulting in lower levels of the modified receptor. This
CC   method is useful for determining whether or not a treatment is effective
CC   in treating schizophrenia by detecting changes in levels of (un)modified
CC   D4R, preferably with antibodies.
XX
SQ   Sequence   387 AA;


  Query Match             99.9%;  Score 2028;  DB 19;  Length 387;
  Best Local Similarity   99.7%;  Pred. No. 1.4e-145;
  Matches  386;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mgnrstadadgllagrgpaagasagasaglagqgaaalvggvlligavlagnslvcvsva 60

Qy      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
           |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db      61 teralqtptnsfimslaaadlllallvlplfvysevqggawllsprlcdalmamdvalct 120

Qy     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 asifnlcaisvdrfvavavplrynrqggsrrqllligatwllsaavaapvlcglndvrgr 180

Qy     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 dpavcrledrdyvvyssvcsfflpcplmlllywatfrglqrwevarraklhgraprrpsg 240

Qy     241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 pgppsptppaprlpqdpcgpdcappapglppdpcgsncappdavraaalppqtppqtrrr 300

Qy     301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 rrakitgrerkamrvlpvvvgafllcwtpffvvhitqalcpacsvpprlvsavtwlgyvn 360
```

```
Qy    361 SALNPVIYTVFNAEFRNVFRKALRACC 387
          |||||||||||||||||||||||||||
Db    361 salnpviytvfnaefrnvfrkalracc 387
```

RESULT 3
AAR70734
ID AAR70734 standard; Protein; 387 AA.
XX
AC AAR70734;
XX
DT 05-AUG-1995 (first entry)
XX
DE Human D4 dopamine receptor.
XX
KW Dopamine receptor; neurotransmitter; dopaminergic;
KW neuroleptic; drug screening.
XX
OS Synthetic.
XX
PN WO9501435-A.
XX
PD 12-JAN-1995.
XX
PF 01-JUN-1994; 94WO-US05986.
XX
PR 01-JUL-1993; 93US-0086439.
XX
PA (UPJO) UPJOHN CO.
XX
PI Chio C, Huff RM;
XX
DR WPI; 1995-060999/08.
DR P-PSDB; AAQ85071.
XX
PT New synthetic gene for dopamine receptor - used to obtain prods.
PT for use in screening assays for activators or inhibitors or
PT assaying dopaminergic drugs.
XX
PS Disclosure; Fig 2A-2F; 36pp; English.
XX
CC The human D4 dopamine receptor is expressed from an artifical gene,
CC and can be used to screen compounds for D4 and dopaminergic
CC activity.
XX
SQ Sequence 387 AA;

Query Match 99.8%; Score 2026; DB 16; Length 387;
Best Local Similarity 99.7%; Pred. No. 2e-145;
Matches 386; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 mgnrstadadgllagrgpaagasagasaglagqgaaalvggvlligavlagnslvcvsva 60

Qy     61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db     61 teralqtptnsfivslaaadlllallvlplfvysevqggawllsprlcdalmamdvmlct 120

Qy    121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 asifnlcaisvdrfvavavplrynrqggsrrqllligatwllsaavaapvlcglndvrgr 180

Qy    181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 dpavcrledrdyvvyssvcsfflpcplmlllywatfrglqrwevarraklhgraprrpsg 240

Qy    241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 pgppsptppaprlpqdpcgpdcappapglppdpcgsncappdavraaalppqtppqtrrr 300

Qy    301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 rrakitgrerkamrvlpvvvgafllcwtpffvvhitqalcpacsvpprlvsavtwlgyvn 360

```
Qy    361 SALNPVIYTVFNAEFRNVFRKALRACC 387
          |||||||||||||||||||||||||||
Db    361 salnpviytvfnaefrnvfrkalracc 387
```

RESULT 4
AAB15760
ID AAB15760 standard; Protein; 387 AA.
XX
AC AAB15760;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human D4 receptor protein.
XX
KW Rat; D4 dopamine receptor; cardiovascular system; retinal tissue;
KW vasoregulator.
XX
OS Homo sapiens.
XX
PN US6121015-A.
XX
PD 19-SEP-2000.
XX
PF 07-JUN-1995; 95US-0475742.
XX
PR 16-JUN-1994; 94US-0261293.
PR 28-JAN-1993; 93US-0014013.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Todd RD, O'Malley KL;
XX
DR WPI; 2000-655527/63.
DR N-PSDB; AAA99602.
XX
PT Screening for compounds that selectively bind to a rat D4 dopamine
PT receptor (DDR), useful for identifying dopamine (ant)agonists,
PT comprises exposing cells transfected with a nucleic acid encoding the
PT DDR to candidate compounds -
XX
PS Disclosure; Column 27-29; 29pp; English.
XX
CC The present sequence is the human D4 dopamine receptor. The rat
CC analogue of the human D4 receptor was isolated from a rat genomic
CC library by PCR and low stringency library screening. A cDNA encoding
CC the rat D4 dopamine receptor was expressed in transfected mammalian cells
CC and shown to preferentially bind dopamine antagonists such as clozapine.
CC The cDNA is useful for screening drugs which specifically bind to the
CC receptor and have selective effects on the cardiovasculature and retinal
CC tissues through interactions with the receptor. Such compounds may act as
CC vasoregulators or may have ionotropic effects. The D4 receptor protein
CC may be used for the production of polyclonal or monoclonal antibodies
CC which recognise the D4 receptor sequence but do not recognise other
CC dopamenergic receptors. The antibodies may be used in
CC immunocytochemical studies and for identification and isolation via
CC flow sorting of D4 expressing cell types.
XX
SQ Sequence 387 AA;

Query Match 99.8%; Score 2026; DB 21; Length 387;
Best Local Similarity 99.7%; Pred. No. 2e-145;
Matches 386; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 mgnrstadadgllagrgpaagasagasaglagqgaaalvggvlligavlagnslvcvsva 60

Qy     61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
```
```

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      61 teralqtptnsfivslaaadlllallvlplfvysevqggawllsprlcdalmamdvmlct 120

Qy     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 asifnlcaisvdrfvavavplrynrqggsrrqllligatwllsaavaapvlcglndvrgr 180

Qy     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 dpavcrledrdyvvyssvcsfflpcplmlllywatfrglqrwevarraklhgraprrpsg 240

Qy     241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 pgppsptppaprlpqdpcgpdcappapglppdpcgsncappdavraaalppqtppqtrrr 300

Qy     301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 rrakitgrerkamrvlpvvvgafllcwtpffvvhitqalcpacsvpprlvsavtwlgyvn 360

Qy     361 SALNPVIYTVFNAEFRNVFRKALRACC 387
           |||||||||||||||||||||||||||
Db     361 salnpviytvfnaefrnvfrkalracc 387


RESULT   5
AAR48948
ID   AAR48948 standard; Protein; 387 AA.
XX
AC   AAR48948;
XX
DT   05-SEP-1994  (first entry)
XX
DE   Sequence encoded by allele D4.2 of the human dopamine receptor.
XX
KW   Dopamine receptor; shizophrenia; manic depression;
KW   genetic disorder; neuropsychiatric disorder; drug; RFLP;
KW   restriction fragment length polymorphism.
XX
OS   Homo sapiens.
XX
PN   WO9403602-A.
XX
PD   17-FEB-1994.
XX
PF   05-AUG-1993;   93WO-US07370.
XX
PR   10-AUG-1992;   92US-0928611.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI   Civelli O,  Vantol HH;
XX
DR   WPI; 1994-065691/08.
DR   N-PSDB; AAQ57655.
XX
PT   DNA encoding human D4 dopamine receptor - used to identify
PT   restriction fragment length polymorphisms associated with genetic
PT   disorders in a population, and to screen drugs for antipsychotic
PT   activity.
XX
PS   Claim 13; Page 42-43; 70pp; English.
XX
CC   Naturally occurring alleles of the human D4 dopamine receptor gene
CC   comprise from about 2 to about 8 copies of a nucleotide sequence
CC   described in AAQ57654 which can be used to screen for restriction
CC   fragment length polymorphisms (RFLP's).  These may be associated
CC   with genetic disorders  and neuropsychiatric disorders e.g.
CC   schizophrenia and manic depression.  The RFLP's may also be used
CC   to predict an individuals response to psychotropic and
CC   antipsychotic drugs.  This sequence is encoded by allele D4.2 of
CC   the human dopamine receptor.
XX
SQ   Sequence   387 AA;
```

```
  Query Match             99.0%;  Score 2011;  DB 15;  Length 387;
  Best Local Similarity   99.2%;  Pred. No. 2.7e-144;
  Matches  384;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       1 mgnrstadadgllagrgraagasagasaglagqgaaalvggvlligavlagnslvcvsva 60

Qy      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      61 teralqtptnsfivslaaadlllallvlplfvysevqggawllsprlcdalmamdvmlct 120

Qy     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 asifnlcaisvdrfvavavplrynrqggsrrqllligatwllsaavaapvlcglndvrgr 180

Qy     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 dpavcrledrdyvvyssvcsfflpcplmlllywatfrglqrwevarraklhgraprrpsg 240

Qy     241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 pgppsptppaprlpqdpcgpdcappapglppdpcgsncappdavraaalppqtppqtrrr 300

Qy     301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 rrakitgrerkamrvlpvvvgafllcwtpffvvhitqalcpacsvpprlvsavtwlgyvn 360

Qy     361 SALNPVIYTVFNAEFRNVFRKALRACC 387
           ||| |||||||||||||||||||||||
Db     361 saltpviytvfnaefrnvfrkalracc 387


RESULT   6
AAR96213
ID   AAR96213 standard; Protein; 387 AA.
XX
AC   AAR96213;
XX
DT   21-NOV-1996  (first entry)
XX
DE   Recombinant human D4 dopamine receptor D4.2.
XX
KW   Dopamine; receptor; mental disorder; neurological; psychotic episode;
KW   schizophrenia; antipsychotic; psychotropic compound; manic depression;
KW   drug screening.
XX
OS   Homo sapiens.
XX
PN   US5516683-A.
XX
PD   14-MAY-1996.
XX
PF   07-DEC-1990;   90US-0626618.
XX
PR   29-APR-1993;   93US-0056051.
PR   07-DEC-1990;   90US-0626618.
PR   10-AUG-1992;   92US-0928611.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI   Bunzow JR,  Civelli O,  Grandy DK,  Van Tol HH;
XX
DR   WPI; 1996-251012/25.
DR   N-PSDB; AAT27545.
XX
PT   Recombinant expression of human D4 dopamine receptor - using a
PT   vaccinia virus vector operably linked to nucleic acid encoding the
PT   receptor in eukaryotic cells
XX
PS   Claim 2; Column 17-20; 38pp; English.
```

```
XX
CC   AAR96213 is a human D4 dopamine receptor, D4.2. A cDNA sequence encoding
CC   D4.2 may be inserted into a vaccinia viral vector (e.g. pZVneo)
CC   and this vector used to transform eukaryotic cells so as to express
CC   a recombinant D4 dopamine receptor (DR). Recombinant D4 DR can be
CC   used for screening potential psychotropic and antipsychotic drugs
CC   which may be useful to treat such conditions as depression and
CC   schizophrenia. Human D4 DR can also be used for the detection of
CC   dopamine or its analogues and for the production of antibodies. D4 DR
CC   is the only known clozapine-sensitive human dopamine receptor, drugs
CC   identified using D4 DR may share clozapines useful property of not
CC   inducing tardive dyskinesia and other motor side effects.
XX
SQ   Sequence   387 AA;


  Query Match             99.0%;  Score 2011;  DB 17;  Length 387;
  Best Local Similarity   99.2%;  Pred. No. 2.7e-144;
  Matches  384;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db      1 mgnrstadadgllagrgraagasagasaglagqgaaalvggvlligavlagnslvcvsva 60

Qy     61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db     61 teralqtptnsfivslaaadlllallvlplfvysevqggawllsprlcdalmamdvmlct 120

Qy    121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 asifnlcaisvdrfvavavplrynrgggsrrqllligatwllsaavaapvlcglndvrgr 180

Qy    181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 dpavcrledrdyvvyssvcsfflpcplmlllywatfrglqrwevarraklhgraprrpsg 240

Qy    241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 pgppsptppaprlpqdpcgpdcappapglppdpcgsncappdavraaalppqtppqtrrr 300

Qy    301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 rrakitgrerkamrvlpvvvgafllcwtpffvvhitqalcpacsvpprlvsavtwlgyvn 360

Qy    361 SALNPVIYTVFNAEFRNVFRKALRACC 387
          ||| |||||||||||||||||||||||
Db    361 saltpviytvfnaefrnvfrkalracc 387


RESULT   7
AAR25335
ID   AAR25335 standard; Protein; 387 AA.
XX
AC   AAR25335;
XX
DT   06-JAN-1993  (first entry)
XX
DE   D4 dopamine receptor.
XX
KW   D2; D3; clozapine; tardive dyskinesia; schizophrenia.
XX
OS   Homo sapiens.
XX
PN   WO9210571-A.
XX
PD   25-JUN-1992.
XX
PF   06-DEC-1991;   91WO-US09308.
XX
PR   07-DEC-1990;   90US-0626618.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI   Civelli O,  Van Tol H;
XX
DR   WPI; 1992-234627/28.
DR   N-PSDB; AAQ25870, AAQ25871 and AAQ25782.
XX
PT   New human dopamine D4 receptor and DNA encoding it - used to
PT   diagnose genetic diseases, expression vectors contg. the DNA are
PT   used to screen antipsychotic drugs
XX
PS   Disclosure; Fig 2; 44pp; English.
XX
CC   The sequence given is the human dopamin D4 receptor.  The receptor
CC   D4 has high homology to the other dopamine receptors D2 and D3.  It
CC   has a ten fold higher affinity for clozapine, an antipsychotic drug
CC   which does not cause tardive dyskinesia or other motor side effects.
CC   This new receptor may prove useful in identifying new drugs for
CC   schizophrenia that have similar properties to clozapine.  This protein
CC   has a molecular weight of 41 kD and can be produced by recombinant DNA
CC   technology.  It can be used for the in vitro screening of novel
CC   antipyscotic compounds.  Cells transformed by the DNA encoding this
CC   protein, to express the receptor which do not usually express it, are
CC   useful for the preparation of cell membranes for receptor binding
CC   assays and drug screening. Competitive binding assays can be used to
CC   identify agonists and antagonists.  The receptor can be used for the
CC   in vivo detection of dopaminergic drugs in solution.
XX
SQ   Sequence   387 AA;


  Query Match             98.9%;  Score 2008;  DB 13;  Length 387;
  Best Local Similarity   99.0%;  Pred. No. 4.5e-144;
  Matches  383;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db      1 mgnrstadadgllagrgraagasagasaglagqgaaalvggvlligavlagnslvcvsva 60

Qy     61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db     61 teralqtptnsfivslaaadlllallvlplfvysevqggawllsprlcdalmamdvmlct 120

Qy    121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 asifnlcaisvdrfvavavplrynrqggsrrqllligatwllsaavaapvlcglndvrgr 180

Qy    181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 dpavcrledrdyvvyssvcsfflpcplmlllywatfrglqrwevarraklhgraprrpsg 240

Qy    241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 pgppsptppaprlpqdpcgpdcappapglppdpcgsncappdavraaalppqtppqtrrr 300

Qy    301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 rrakitgrerkamrvlpvvvgafllcwtpffvvhitqalcpacsvpprlvsavtwlgyvn 360

Qy    361 SALNPVIYTVFNAEFRNVFRKALRACC 387
          :|| |||||||||||||||||||||||
Db    361 naltpviytvfnaefrnvfrkalracc 387


RESULT   8
AAR75957
ID   AAR75957 standard; Protein; 387 AA.
XX
AC   AAR75957;
XX
DT   22-DEC-1995  (first entry)
XX
DE   Human dopamine D4 receptor.
XX
KW   Restriction fragment length polymorphism; RFLP; point mutation;
```

```
KW   mapping; dopamine D4 receptor; DRD4.
XX
OS   Homo sapiens.
XX
PN   CA2136705-A.
XX
PD   27-MAY-1995.
XX
PF   25-NOV-1994;   94CA-2136705.
XX
PR   26-NOV-1993;   93US-0157269.
XX
PA   (CLAR-) CLARKE INST PSYCHIATRY.
XX
PI   Kennedy JL,  Petronis A;
XX
DR   WPI; 1995-255407/34.
XX
PT   Screening for polymorphism by amplification of pooled nucleic acid
PT   - restriction with endonuclease(s), sepn. of fragments and
PT   comparison of restriction patterns, for detecting disease related
PT   mutation(s), in genetic mapping etc.
XX
PS   Example 1; Fig.5; 48pp; English.
XX
CC   A 0.7 kb fragment in the DRD4 gene including the first exon was
CC   amplified in pooled DNA from 14 individuals by PCR.  The direct
CC   primer (given in AAQ91530) was derived from nt -421 to 402, and the
CC   reverse primer (AAQ91531) from nt 286 to 267.  Examination of
CC   restriction digests of the PCR product revealed a new 2-allele
CC   SmaI RFLP.  The full DRD4 gene is given in AAQ91532.
XX
SQ   Sequence   387 AA;


  Query Match             98.1%;  Score 1993;  DB 16;  Length 387;
  Best Local Similarity   99.0%;  Pred. No. 6.1e-143;
  Matches  384;  Conservative    0;  Mismatches    2;  Indels    2;  Gaps    2;

Qy       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mgnrstadadgllagrgpaagasagasaglagqgaaalvggvlligavlagnslvcvsva 60

Qy      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      61 teralqtptnsfivslaaadlllallvlplfvysevqggawllsprlcdalmamdvmlct 120

Qy     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
            |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db     121 -sifnlcaisvdrfvavavplrynrqggsrrqllligatwllsaavaapvlcklndvrgr 179

Qy     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARR-AKLHGRAPRRPS 239
           ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db     180 dpavcrledrdyvvyssvcsfflpcplmlllywatfrglqrwevarraaklhgraprrps 239

Qy     240 GPGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRR 299
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     240 gpgppsptppaprlpqdpcgpdcappapglppdpcgsncappdavraaalppqtppqtrr 299

Qy     300 RRRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYV 359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     300 rrrakitgrerkamrvlpvvvgafllcwtpffvvhitqalcpacsvpprlvsavtwlgyv 359

Qy     360 NSALNPVIYTVFNAEFRNVFRKALRACC 387
           ||||||||||||||||||||||||||||
Db     360 nsalnpviytvfnaefrnvfrkalracc 387


RESULT   9
AAW01749
ID   AAW01749 standard; protein; 387 AA.
XX
AC   AAW01749;
XX
DT   17-MAY-1997  (first entry)
XX
DE   Human dopamine D4 receptor.
XX
KW   Dopamine D4 receptor; biochemical abnormality; methionine metabolism;
KW   schizophrenia; neurotransmission; methionine residue 313; adenosyl;
KW   methionine adenosyltransferase; MAT; assay; diagnosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          34..54
FT                   /label= transmembrane_spanning_domain
FT   Domain          75..96
FT                   /label= transmembrane_spanning_domain
FT   Domain          110..129
FT                   /label= transmembrane_spanning_domain
FT   Domain          152..172
FT                   /label= transmembrane_spanning_domain
FT   Domain          192..211
FT                   /label= transmembrane_spanning_domain
FT   Domain          315..335
FT                   /label= transmembrane_spanning_domain
FT   Domain          351..371
FT                   /label= transmembrane_spanning_domain
FT   Modified-site   313
FT                   /note= "hot-spot; possible modification with adenosyl"
XX
PN   WO9637780-A1.
XX
PD   28-NOV-1996.
XX
PF   14-MAY-1996;   96WO-US06863.
XX
PR   24-MAY-1995;   95US-0449153.
XX
PA   (DETH/) DETH R C.
XX
PI   Deth RC;
XX
DR   WPI; 1997-021349/02.
XX
PT   Diagnosis and treatment of schizophrenia - using biochemical assays
PT   based on a modified dopamine D4 receptor or methionine
PT   adenosyl:transferase activities
XX
PS   Disclosure; Fig 2; 38pp; English.
XX
CC   The present sequence is that of the human dopamine D4 receptor. It has
CC   been discovered that a biochemical abnormality in methionine metabolism
CC   associated with schizophrenia is linked to the clinical manifestations
CC   of altered dopamine neurotransmission. The dopamine receptor is abnormal
CC   in schizophrenics, in that methionine residue 313 is abnormally modified.
CC   In normal individuals Met313 is modified by the addition of an adenosyl
CC   group to Its sulfur atom via the action of methionine adenosyltransferase
CC   (MAT). Individuals with schizophrenia are deficient in MAT activity, and
CC   therefore have a lower amount of the modified dopamine D4 receptor. This
CC   fact is used in a claimed biochemical assay for diagnosis of
CC   schizophrenia.
XX
SQ   Sequence   387 AA;


  Query Match             98.1%;  Score 1993;  DB 18;  Length 387;
  Best Local Similarity   99.0%;  Pred. No. 6.1e-143;
  Matches  384;  Conservative    0;  Mismatches    2;  Indels    2;  Gaps    2;

Qy       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mgnrstadadgllagrgpaagasagasaglagqgaaalvggvlligavlagnslvcvsva 60

Qy      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
```

```
Db     61 teralqtptnsfivslaaadlllallvlplfvysevqggawllsprlcdalmamdvmlct 120

Qy    121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db    121 -sifnlcaisvdrfvavavplrynrqggsrrqllligatwllsaavaapvlcklndvrgr 179

Qy    181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARR-AKLHGRAPRRPS 239
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    180 dpavcrledrdyvvyssvcsfflpcplmlllywatfrglqrwevarraaklhgraprrps 239

Qy    240 GPGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRR 299
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    240 gpgppsptppaprlpqdpcgpdcappapglppdpcgsncappdavraaalppqtppqtrr 299

Qy    300 RRRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYV 359
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300 rrrakitgrerkamrvlpvvvgafllcwtpffvvhitqalcpacsvpprlvsavtwlgyv 359

Qy    360 NSALNPVIYTVFNAEFRNVFRKALRACC 387
          |||||||||||||||||||||||||||||
Db    360 nsalnpviytvfnaefrnvfrkalracc 387


RESULT  10
AAR48949
ID   AAR48949 standard; Protein; 419 AA.
XX
AC   AAR48949;
XX
DT   05-SEP-1994  (first entry)
XX
DE   Sequence encoded by allele D4.4 of the human dopamine receptor.
XX
KW   Dopamine receptor; shizophrenia; manic depression;
KW   genetic disorder; neuropsychiatric disorder; drug; RFLP;
KW   restriction fragment length polymorphism.
XX
OS   Homo sapiens.
XX
PN   WO9403602-A.
XX
PD   17-FEB-1994.
XX
PF   05-AUG-1993;   93WO-US07370.
XX
PR   10-AUG-1992;   92US-0928611.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI   Civelli O,  Vantol HH;
XX
DR   WPI; 1994-065691/08.
DR   N-PSDB; AAQ57656.
XX
PT   DNA encoding human D4 dopamine receptor - used to identify
PT   restriction fragment length polymorphisms associated with genetic
PT   disorders in a population, and to screen drugs for antipsychotic
PT   activity.
XX
PS   Claim 14; Page 46-47; 70pp; English.
XX
CC   Naturally occurring alleles of the human D4 dopamine receptor gene
CC   comprise from about 2 to about 8 copies of a nucleotide sequence
CC   described in AAQ57654 which can be used to screen for restriction
CC   fragment length polymorphisms (RFLP's).  These may be associated
CC   with genetic disorders  and neuropsychiatric disorders e.g.
CC   schizophrenia and manic depression.  The RFLP's may also be used
CC   to predict an individuals response to psychotropic and
CC   antipsychotic drugs.  This sequence is encoded by allele D4.4 of
CC   the human dopamine receptor.
XX
SQ   Sequence   419 AA;
```

```
  Query Match             97.7%;  Score 1985;  DB 15;  Length 419;
  Best Local Similarity   91.6%;  Pred. No. 2.7e-142;
  Matches  384;  Conservative    0;  Mismatches   3;  Indels   32;  Gaps    1;

Qy      1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db      1 mgnrstadadgllagrgraagasagasaglagqgaaalvggvlligavlagnslvcvsva 60

Qy     61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db     61 teralqtptnsfivslaaadlllallvlplfvysevqggawllsprlcdalmamdvmlct 120

Qy    121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 asifnlcaisvdrfvavavplrynrqggsrrqllligatwllsaavaapvlcglndvrgr 180

Qy    181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 dpavcrledrdyvvyssvcsfflpcplmlllywatfrglqrwevarraklhgraprrpsg 240

Qy    241 PGPPSPTPPAPR------------------------------LPQDPCGPDCAPPAPG 268
          ||||||||||||                              ||||||||||||||||
Db    241 pgppsptppaprlpqdpcgpdcappapglprgpcgpdcapaapslpqdpcgpdcappapg 300

Qy    269 LPPDPCGSNCAPPDAVRAAALPPQTPPQTRRRRRAKITGRERKAMRVLPVVVGAFLLCWT 328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 lppdpcgsncappdavraaalppqtppqtrrrrrakitgrerkamrvlpvvvgafllcwt 360

Qy    329 PFFVVHITQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKALRACC 387
          ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    361 pffvvhitqalcpacsvpprlvsavtwlgyvnsaltpviytvfnaefrnvfrkalracc 419


RESULT  11
AAR96214
ID   AAR96214 standard; Protein; 419 AA.
XX
AC   AAR96214;
XX
DT   21-NOV-1996  (first entry)
XX
DE   Recombinant human D4 dopamine receptor D4.4.
XX
KW   Dopamine; receptor; mental disorder; neurological; psychotic episode;
KW   schizophrenia; antipsychotic; psychotropic compound; manic depression;
KW   drug screening.
XX
OS   Homo sapiens.
XX
PN   US5516683-A.
XX
PD   14-MAY-1996.
XX
PF   07-DEC-1990;   90US-0626618.
XX
PR   29-APR-1993;   93US-0056051.
PR   07-DEC-1990;   90US-0626618.
PR   10-AUG-1992;   92US-0928611.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI   Bunzow JR,  Civelli O,  Grandy DK,  Van Tol HH;
XX
DR   WPI; 1996-251012/25.
DR   N-PSDB; AAT27546.
XX
PT   Recombinant expression of human D4 dopamine receptor - using a
PT   vaccinia virus vector operably linked to nucleic acid encoding the
PT   receptor in eukaryotic cells
XX
PS   Claim 3; Column 23-24; 38pp; English.
```

```
XX
CC   AAR96214 is a human D4 dopamine receptor, D4.4. A cDNA sequence encoding
CC   D4.4 may be inserted into a vaccinia viral vector (e.g. pZVneo)
CC   and this vector used to transform eukaryotic cells so as to express
CC   a recombinant D4 dopamine receptor (DR). Recombinant D4 DR can be
CC   used for screening potential psychotropic and antipsychotic drugs
CC   which may be useful to treat such conditions as depression and
CC   schizophrenia. Human D4 DR can also be used for the detection of
CC   dopamine or its analogues and for the production of antibodies. D4 DR
CC   is the only known clozapine-sensitive human dopamine receptor, drugs
CC   identified using D4 DR may share clozapines useful property of not
CC   inducing tardive dyskinesia and other motor side effects.
XX
SQ   Sequence   419 AA;


  Query Match             97.7%;  Score 1985;  DB 17;  Length 419;
  Best Local Similarity   91.6%;  Pred. No. 2.7e-142;
  Matches  384;  Conservative    0;  Mismatches    3;  Indels   32;  Gaps    1;

Qy       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       1 mgnrstadadgllagrgraagasagasaglagqgaaalvggvlligavlagnslvcvsva 60

Qy      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      61 teralqtptnsfivslaaadlllallvlplfvysevqggawllsprlcdalmamdvmlct 120

Qy     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 asifnlcaisvdrfvavavplrynrqggsrrqllligatwllsaavaapvlcglndvrgr 180

Qy     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 dpavcrledrdyvvyssvcsfflpcplmlllywatfrglqrwevarraklhgraprrpsg 240

Qy     241 PGPPSPTPPAPR--------------------------------LPQDPCGPDCAPPAPG 268
           ||||||||||||                                ||||||||||||||||
Db     241 pgppsptppaprlpqdpcgpdcappapglprgpcgpdcapaapslpqdpcgpdcappapg 300

Qy     269 LPPDPCGSNCAPPDAVRAAALPPQTPPQTRRRRRAKITGRERKAMRVLPVVVGAFLLCWT 328
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 lppdpcgsncappdavraaalppqtppqtrrrrrakitgrerkamrvlpvvvgafllcwt 360

Qy     329 PFFVVHITQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKALRACC 387
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     361 pffvvhitqalcpacsvpprlvsavtwlgyvnsaltpviytvfnaefrnvfrkalracc 419


RESULT  12
AAR48950
ID   AAR48950 standard; Protein; 467 AA.
XX
AC   AAR48950;
XX
DT   05-SEP-1994  (first entry)
XX
DE   Sequence encoded by allele D4.7 of the human dopamine receptor.
XX
KW   Dopamine receptor; shizophrenia; manic depression;
KW   genetic disorder; neuropsychiatric disorder; drug; RFLP;
KW   restriction fragment length polymorphism.
XX
OS   Homo sapiens.
XX
PN   WO9403602-A.
XX
PD   17-FEB-1994.
XX
PF   05-AUG-1993;   93WO-US07370.
XX
PR   10-AUG-1992;   92US-0928611.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI   Civelli O,  Vantol HH;
XX
DR   WPI; 1994-065691/08.
DR   N-PSDB; AAQ57657.
XX
PT   DNA encoding human D4 dopamine receptor - used to identify
PT   restriction fragment length polymorphisms associated with genetic
PT   disorders in a population, and to screen drugs for antipsychotic
PT   activity.
XX
PS   Claim 15; Page 50-51; 70pp; English.
XX
CC   Naturally occurring alleles of the human D4 dopamine receptor gene
CC   comprise from about 2 to about 8 copies of a nucleotide sequence
CC   described in AAQ57654 which can be used to screen for restriction
CC   fragment length polymorphisms (RFLP's).  These may be associated
CC   with genetic disorders  and neuropsychiatric disorders e.g.
CC   schizophrenia and manic depression.  The RFLP's may also be used
CC   to predict an individuals response to psychotropic and
CC   antipsychotic drugs.  This sequence is encoded by allele D4.7 of
CC   the human dopamine receptor.
XX
SQ   Sequence   467 AA;


  Query Match             96.6%;  Score 1961;  DB 15;  Length 467;
  Best Local Similarity   82.2%;  Pred. No. 2e-140;
  Matches  384;  Conservative    0;  Mismatches    3;  Indels   80;  Gaps    1;

Qy       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       1 mgnrstadadgllagrgraagasagasaglagqgaaalvggvlligavlagnslvcvsva 60

Qy      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      61 teralqtptnsfivslaaadlllallvlplfvysevqggawllsprlcdalmamdvmlct 120

Qy     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 asifnlcaisvdrfvavavplrynrqggsrrqllligatwllsaavaapvlcglndvrgr 180

Qy     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 dpavcrledrdyvvyssvcsfflpcplmlllywatfrglqrwevarraklhgraprrpsg 240

Qy     241 PGPPSPTPPAPR---------------------------------------------- 252
           ||||||||||||
Db     241 pgppsptppaprlpqdpcgpdcappapglprgpcgpdcapaapglppdpcgpdcappapg 300

Qy     253 -------------------------------LPQDPCGPDCAPPAPGLPPDPCGSNCAP 280
                                           ||||||||||||||||||||||||||||
Db     301 lpqdpcgpdcappapglprgpcgpdcappapglpqdpcgpdcappapglppdpcgsncap 360

Qy     281 PDAVRAAALPPQTPPQTRRRRRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALC 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 pdavraaalppqtppqtrrrrrakitgrerkamrvlpvvvgafllcwtpffvvhitqalc 420

Qy     341 PACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKALRACC 387
           |||||||||||||||||||| ||||||||||||||||||||||||||
Db     421 pacsvpprlvsavtwlgyvnsaltpviytvfnaefrnvfrkalracc 467


RESULT  13
AAR96215
ID   AAR96215 standard; Protein; 467 AA.
XX
AC   AAR96215;
XX
DT   21-NOV-1996  (first entry)
XX
DE   Recombinant human D4 dopamine receptor D4.7.
```

```
XX
KW   Dopamine; receptor; mental disorder; neurological; psychotic episode;
KW   schizophrenia; antipsychotic; psychotropic compound; manic depression;
KW   drug screening.
XX
OS   Homo sapiens.
XX
PN   US5516683-A.
XX
PD   14-MAY-1996.
XX
PF   07-DEC-1990;   90US-0626618.
XX
PR   29-APR-1993;   93US-0056051.
PR   07-DEC-1990;   90US-0626618.
PR   10-AUG-1992;   92US-0928611.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI   Bunzow JR,  Civelli O,  Grandy DK,  Van Tol HH;
XX
DR   WPI; 1996-251012/25.
DR   N-PSDB; AAT27547.
XX
PT   Recombinant expression of human D4 dopamine receptor - using a
PT   vaccinia virus vector operably linked to nucleic acid encoding the
PT   receptor in eukaryotic cells
XX
PS   Claim 4; Column 29-32; 38pp; English.
XX
CC   AAR96215 is a human D4 dopamine receptor, D4.7. A cDNA sequence encoding
CC   D4.7 may be inserted into a vaccinia viral vector (e.g. pZVneo)
CC   and this vector used to transform eukaryotic cells so as to express
CC   a recombinant D4 dopamine receptor (DR). Recombinant D4 DR can be
CC   used for screening potential psychotropic and antipsychotic drugs
CC   which may be useful to treat such conditions as depression and
CC   schizophrenia. Human D4 DR can also be used for the detection of
CC   dopamine or its analogues and for the production of antibodies. D4 DR
CC   is the only known clozapine-sensitive human dopamine receptor, drugs
CC   identified using D4 DR may share clozapines useful property of not
CC   inducing tardive dyskinesia and other motor side effects.
XX
SQ   Sequence   467 AA;


  Query Match             96.6%;  Score 1961;  DB 17;  Length 467;
  Best Local Similarity   82.2%;  Pred. No. 2e-140;
  Matches  384;  Conservative    0;  Mismatches    3;  Indels   80;  Gaps    1;

Qy       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
           |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db       1 mgnrstadadgllagrgraagasagasaglagqgaaalvggvlligavlagnslvcvsva 60

Qy      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      61 teralqtptnsfivslaaadlllallvlplfvysevqggawllsprlcdalmamdvmlct 120

Qy     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 asifnlcaisvdrfvavavplrynrqggsrrqllligatwllsaavaapvlcglndvrgr 180

Qy     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 dpavcrledrdyvvyssvcsfflpcplmlllywatfrglqrwevarraklhgraprrpsg 240

Qy     241 PGPPSPTPPAPR---------------------------------------------- 252
           ||||||||||||
Db     241 pgppsptppaprlpqdpcgpdcappapglprgpcgpdcapaapglppdpcgpdcappapg 300

Qy     253 ------------------------------LPQDPCGPDCAPPAPGLPPDPCGSNCAP 280
                                           ||||||||||||||||||||||||||||
Db     301 lpqdpcgpdcappapglprgpcgpdcappapglpqdpcgpdcappapglppdpcgsncap 360

Qy     281 PDAVRAAALPPQTPPQTRRRRRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALC 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 pdavraaalppqtppqtrrrrrakitgrerkamrvlpvvvgafllcwtpffvvhitqalc 420

Qy     341 PACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKALRACC 387
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RESULT  14
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ID   AAR48707 standard; Protein; 315 AA.
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AC   AAR48707;
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DT   05-JUN-1996  (first entry)
XX
DE   G-protein coupled human dopamine D4 receptor protein.
XX
KW   G-protein coupled receptor; ligand binding assay; transmembrane domain;
KW   psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin;
KW   muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;
KW   rhodopsin; opsin; odorant; cytomegalovirus.
XX
OS   Homo sapiens.
XX
PN   WO9405695-A1.
XX
PD   17-MAR-1994.
XX
PF   09-SEP-1993;   93WO-US08528.
XX
PR   10-SEP-1992;   92US-0943236.
XX
PA   (UYNY ) UNIV NEW YORK STATE.
XX
PI   Murphy RB,  Schuster DI;
XX
DR   WPI; 1994-101120/12.
XX
PT   Polypeptides of G-coupled receptor proteins (GPRs) - useful for
PT   binding GPR ligands or modulating GPR binding
XX
PS   Disclosure; Page 81; 160pp; English.
XX
CC   Proteins AAR48685-R48758 represent a range of G-protein coupled receptor
CC   proteins selected from cAMP, adenosine, muscarinic acetylcholine,
CC   adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
CC   odorant, cytomegaloviral and other G-protein coupled receptors.  The
CC   receptor proteins were used to design polypeptides, pref. based on the
CC   transmembrane domains, for use in G-protein coupled receptor ligand
CC   binding assays.  The polypeptide fragments retain biological activity
CC   such as binding a GPR ligand or modulating GPR ligand binding to a GPR
CC   (see AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples
CC   of polypeptide fragments).  The polypeptide fragments can be used in
CC   compositions for treating subjects suffering from a pathology related to
CC   a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
XX
SQ   Sequence   315 AA;


  Query Match             76.2%;  Score 1548.5;  DB 15;  Length 315;
  Best Local Similarity   87.0%;  Pred. No. 1.9e-109;
  Matches  308;  Conservative    2;  Mismatches    5;  Indels   39;  Gaps    4;

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Qy      94 SEVQGGAWLLSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQL 153
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Db      61 sevqgaawllsprlc------dvmlctasifnlcaisvdrfvavavplrynrqggsrrql 114
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Qy    154 LLIGATWLLSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYW 213
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Qy    214 ATFRGLQRWEVARRAKLHGRAPRRPSGPGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDP 273
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Qy    274 CGSNCAPPDAVRAAALPPQTPPQTRRRRRAKITGRERKAMRVLPVVVGAFLLCWTPFFVV 333
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Qy    334 HITQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKALRACC 387
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Db    262 hitqalcpacsvpprlvsavtwlsyvnsainpviytvfnaefrnvfrkalracc 315
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RESULT 15
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ID AAW02679 standard; peptide; 315 AA.
XX
AC AAW02679;
XX
DT 12-NOV-1996 (first entry)
XX
DE G-protein coupled human dopamine D4 receptor.
XX
KW G-protein coupled receptor; ligand binding assay; transmembrane domain;
KW schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin;
KW muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;
KW odorant; cytomegalovirus; serotonergic.
XX
OS Homo sapiens.
XX
PN US5508384-A.
XX
PD 16-APR-1996.
XX
PF 10-SEP-1992; 92US-0943236.
XX
PR 09-SEP-1993; 93US-0118270.
PR 10-SEP-1992; 92US-0943236.
XX
PA (UYNY) UNIV NEW YORK STATE.
XX
PI Murphy RB, Schuster DI;
XX
DR WPI; 1996-208785/21.
XX
PT New dopamine receptor peptide - useful as antipsychotic agent, e.g.
PT for treating schizophrenia
XX
PS Disclosure; Column 85-88; 184pp; English.
XX
CC Proteins AAW02657-W02730 represent a range of G-protein coupled receptor
CC (GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine,
CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
CC odorant, cytomegaloviral and other GPR proteins. The receptor proteins
CC were used to design polypeptides, pref. based on the transmembrane
CC domains, for use in G-protein coupled receptor ligand binding assays.
CC The polypeptide fragments retain biological activity such as binding a
CC GPR ligand or modulating GPR ligand binding to a GPR (see
CC AAW02747-W02999 for examples of polypeptide fragments). The polypeptide
CC fragments can be used in compositions for treating subjects suffering
CC from a pathology related to a GPR abnormality e.g. a psychotic disorder
CC such as schizophrenia.
XX
SQ Sequence 315 AA;

Query Match 76.2%; Score 1548.5; DB 17; Length 315;
Best Local Similarity 87.0%; Pred. No. 1.9e-109;
Matches 308; Conservative 2; Mismatches 5; Indels 39; Gaps 4;

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Qy     94 SEVQGGAWLLSPRLCDALMAMDVALCTASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQL 153
          ||||| |||||||||      || ||||||||||||||||||||||||||||||||||||
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Qy    154 LLIGATWLLSAAVAAPVLCGLNDVRGRDPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYW 213
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Db    115 lligatwllsaavaapvlcglndvrgrdpavcrledrdyvvyssvcsfflpcp---llyw 171

Qy    214 ATFRGLQRWEVARRAKLHGRAPRRPSGPGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDP 273
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Db    172 atfrglql--varraklhgraprrpsgpgppsptppaprlpqdpcg-------------- 215

Qy    274 CGSNCAPPDAVRAAALPPQTPPQTRRRRRAKITGRERKAMRVLPVVVGAFLLCWTPFFVV 333
                      ||||||||||||||||||||||||||||||||||||:|||||||||
Db    216 --------------alppqtppqtrrrrrakitgrerkamrvlpvvvgafilcwtpffvv 261

Qy    334 HITQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKALRACC 387
          |||||||||||||||||||| ||||||:||||||||||||||||||||||
Db    262 hitqalcpacsvpprlvsavtwlsyvnsainpviytvfnaefrnvfrkalracc 315
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Job time: 119 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: February 13, 2002, 17:37:14 ; Search time 12.69 Seconds
(without alignments)
686.271 Million cell updates/sec

Title: US-09-550-103-1
Perfect score: 2031
Sequence: 1 MGNRSTADADGLLAGRGPAA.....YTVFNAEFRNVFRKALRACC 387

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2031	100.0	387	3	US-08-833-703-1	Sequence 1, Appli
2	2028	99.9	387	1	US-08-449-153-1	Sequence 1, Appli
3	2028	99.9	387	1	US-08-449-651-1	Sequence 1, Appli
4	2026	99.8	387	1	US-08-086-439C-3	Sequence 3, Appli
5	2026	99.8	387	1	US-08-434-877-3	Sequence 3, Appli
6	2026	99.8	387	3	US-08-475-742-4	Sequence 4, Appli
7	2017	99.3	387	1	US-07-626-618A-17	Sequence 17, Appl
8	2017	99.3	387	1	US-08-333-977-17	Sequence 17, Appl
9	2011	99.0	387	1	US-08-056-051-2	Sequence 2, Appli
10	2011	99.0	387	1	US-07-928-611-18	Sequence 18, Appl
11	2011	99.0	387	2	US-08-487-811A-18	Sequence 18, Appl
12	2011	99.0	387	4	US-09-060-694-18	Sequence 18, Appl
13	2011	99.0	387	5	PCT-US93-07370-18	Sequence 18, Appl
14	1985	97.7	419	1	US-08-056-051-4	Sequence 4, Appli
15	1985	97.7	419	1	US-07-928-611-20	Sequence 20, Appl
16	1985	97.7	419	2	US-08-487-811A-20	Sequence 20, Appl
17	1985	97.7	419	4	US-09-060-694-20	Sequence 20, Appl
18	1985	97.7	419	5	PCT-US93-07370-20	Sequence 20, Appl
19	1961	96.6	467	1	US-08-056-051-6	Sequence 6, Appli
20	1961	96.6	467	1	US-07-928-611-22	Sequence 22, Appl
21	1961	96.6	467	2	US-08-487-811A-22	Sequence 22, Appl
22	1961	96.6	467	4	US-09-060-694-22	Sequence 22, Appl
23	1961	96.6	467	5	PCT-US93-07370-22	Sequence 22, Appl
24	1548.5	76.2	315	1	US-08-118-270-28	Sequence 28, Appl
25	1548.5	76.2	315	5	PCT-US93-08528-28	Sequence 28, Appl
26	1471	72.4	385	3	US-08-475-742-2	Sequence 2, Appli
27	1016	50.0	187	1	US-07-928-611-9	Sequence 9, Appli
28	1016	50.0	187	2	US-08-487-811A-9	Sequence 9, Appli
29	1016	50.0	187	4	US-09-060-694-9	Sequence 9, Appli
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35	966	47.6	267	1	US-07-928-611-13	Sequence 13, Appl
36	966	47.6	267	2	US-08-487-811A-13	Sequence 13, Appl
37	966	47.6	267	4	US-09-060-694-13	Sequence 13, Appl
38	966	47.6	267	5	PCT-US93-07370-13	Sequence 13, Appl
39	744	36.6	136	1	US-07-626-618A-9	Sequence 9, Appli
40	744	36.6	136	1	US-08-333-977-9	Sequence 9, Appli
41	683	33.6	446	1	US-07-781-254A-2	Sequence 2, Appli
42	683	33.6	446	1	US-07-781-254A-3	Sequence 3, Appli
43	679	33.4	444	1	US-07-626-618A-20	Sequence 20, Appl
44	679	33.4	444	1	US-08-333-977-20	Sequence 20, Appl
45	645	31.8	443	1	US-07-626-618A-18	Sequence 18, Appl

ALIGNMENTS

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RESULT   1
US-08-833-703-1
; Sequence 1, Application US/08833703
; Patent No. 6080549
;  GENERAL INFORMATION:
;    APPLICANT:  DETH, RICHARD
;    TITLE OF INVENTION:  METHODS AND MATERIALS FOR THE DIAGNOSIS AND
;    TITLE OF INVENTION:  TREATMENT OF SCHIZOPHRENIA AND RELATED DISORDERS
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Weingarten, Schurgin, Gagnebin & Hayes
;      STREET:  Ten Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/833,703
;      FILING DATE:  08-APR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Heine, Ph.D., Holliday C
;      REGISTRATION NUMBER:  34,346
;      REFERENCE/DOCKET NUMBER:  NU-431XX
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-542 2290
;      TELEFAX:  617-451 0313
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  387 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-833-703-1


  Query Match             100.0%;  Score 2031;  DB 3;  Length 387;
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Db    121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180

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RESULT   2
US-08-449-153-1
; Sequence 1, Application US/08449153
; Patent No. 5686255
;  GENERAL INFORMATION:
;    APPLICANT:  Deth, Richard C.
;    TITLE OF INVENTION:  Compositions and Methods for Diagnosing
;    TITLE OF INVENTION:  Schizophrenia
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/449,153
;      FILING DATE:  24-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carroll, Alice O.
;      REGISTRATION NUMBER:  33,542
;      REFERENCE/DOCKET NUMBER:  RCD95-02
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  387 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-449-153-1


  Query Match           99.9%;  Score 2028;  DB 1;  Length 387;
  Best Local Similarity   99.7%;  Pred. No. 8.3e-114;
  Matches  386;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
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Db    181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240

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RESULT   3
US-08-449-651-1
; Sequence 1, Application US/08449651
; Patent No. 5738998
;  GENERAL INFORMATION:
;    APPLICANT:  Deth, Richard C.
;    TITLE OF INVENTION:  Compositions and Methods for Diagnosing
;    TITLE OF INVENTION:  Schizophrenia
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/449,651
;      FILING DATE:  24-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carroll, Alice O.
;      REGISTRATION NUMBER:  33,542
;      REFERENCE/DOCKET NUMBER:  RCD95-02
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  387 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-449-651-1


  Query Match           99.9%;  Score 2028;  DB 1;  Length 387;
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  Matches  386;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
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Db     301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360

Qy     361 SALNPVIYTVFNAEFRNVFRKALRACC 387
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Db     361 SALNPVIYTVFNAEFRNVFRKALRACC 387


RESULT   4
US-08-086-439C-3
; Sequence 3, Application US/08086439C
; Patent No. 5468615
;  GENERAL INFORMATION:
;    APPLICANT:  Chio, Christopher L.
;    APPLICANT:  Huff, Rita M.
;    TITLE OF INVENTION:  A Synthetic Gene for D4 Dopamine
;    TITLE OF INVENTION:  Receptors
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  The Upjohn Company, Corp. Intellectual
;      ADDRESSEE:  Property Law
;      STREET:  301 Henrietta Street
;      CITY:  Kalamazoo
;      STATE:  Michigan
;      COUNTRY:  USA
;      ZIP:  49001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/086,439C
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Darnley Jr., James D.
;      REGISTRATION NUMBER:  33,673
;      REFERENCE/DOCKET NUMBER:  4700
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  616-385-5210
;      TELEFAX:  616-385-6897
;      TELEX:  224401
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  387 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-086-439C-3


  Query Match             99.8%;  Score 2026;  DB 1;  Length 387;
  Best Local Similarity   99.7%;  Pred. No. 1.1e-113;
  Matches  386;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
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Db       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60

Qy      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
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Db      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVMLCT 120

Qy     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
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Db     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180

Qy     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
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Db     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240

Qy     241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300
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Db     241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300

Qy     301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360
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Db     301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360

Qy     361 SALNPVIYTVFNAEFRNVFRKALRACC 387
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Db     361 SALNPVIYTVFNAEFRNVFRKALRACC 387


RESULT   5
US-08-434-877-3
; Sequence 3, Application US/08434877
; Patent No. 5721132
;  GENERAL INFORMATION:
;    APPLICANT:  Chio, Christopher L.
;    APPLICANT:  Huff, Rita M.
;    TITLE OF INVENTION:  A Synthetic Gene for D4 Dopamine
;    TITLE OF INVENTION:  Receptors
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  The Upjohn Company, Corp. Intellectual
;      ADDRESSEE:  Property Law
;      STREET:  301 Henrietta Street
;      CITY:  Kalamazoo
;      STATE:  Michigan
;      COUNTRY:  USA
;      ZIP:  49001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette (DS,HD)
;      COMPUTER:  Gateway 2000, P5-90
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/434,877
;      FILING DATE:  1 July 1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Darnley Jr., James D.
;      REGISTRATION NUMBER:  33,673
;      REFERENCE/DOCKET NUMBER:  4700 DV1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  616-385-5210
;      TELEFAX:  616-385-6897
;      TELEX:  224401
;  INFORMATION FOR SEQ ID NO:  3:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  387 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-434-877-3


  Query Match             99.8%;  Score 2026;  DB 1;  Length 387;
  Best Local Similarity   99.7%;  Pred. No. 1.1e-113;
  Matches  386;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60

Qy      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVMLCT 120

Qy     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180

Qy     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240

Qy     241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300

Qy     301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360
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Db     301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360

Qy     361 SALNPVIYTVFNAEFRNVFRKALRACC 387
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Db     361 SALNPVIYTVFNAEFRNVFRKALRACC 387


RESULT   6
US-08-475-742-4
; Sequence 4, Application US/08475742
; Patent No. 6121015
; GENERAL INFORMATION:
;  APPLICANT: O'Malley, Karen L
;  APPLICANT: Todd, Richard D
;  TITLE OF INVENTION: Gene Encoding the Rat Dopamine D4 Receptor
;  FILE REFERENCE: WU 102 CON DIV
;  CURRENT APPLICATION NUMBER: US/08/475,742
;  CURRENT FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: US 08/261,293
;  EARLIER FILING DATE: 1994-06-16
;  EARLIER APPLICATION NUMBER: US 08/014,013
;  EARLIER FILING DATE: 1993-01-28
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (1)..(387)
;   OTHER INFORMATION: Human D4 Receptor Protein
US-08-475-742-4


  Query Match             99.8%;  Score 2026;  DB 3;  Length 387;
  Best Local Similarity   99.7%;  Pred. No. 1.1e-113;
  Matches  386;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60

Qy      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVMLCT 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVMLCT 120

Qy     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180

Qy     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240

Qy     241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300
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Db     241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300

Qy     301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360
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Db     301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360

Qy     361 SALNPVIYTVFNAEFRNVFRKALRACC 387
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Db     361 SALNPVIYTVFNAEFRNVFRKALRACC 387


RESULT   7
US-07-626-618A-17
; Sequence 17, Application US/07626618A
; Patent No. 5422265
; GENERAL INFORMATION:
;    APPLICANT:  Van Tol, Hubert H.M.
;    APPLICANT:  Civelli, Olivier
;    TITLE OF INVENTION:  A No. 5422265el Human Dopamine Receptor and Uses
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Allegretti & Witcoff, Ltd.
;      STREET:  10 South Wacker Drive, Suite 3000
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/626,618A
;      FILING DATE:  7 DEC 1990
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5422265nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  90,1092
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-715-1000
;      TELEFAX:  312-715-1234
;      TELEX:  810-221-8317
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  387 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
US-07-626-618A-17
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  Query Match             99.3%;  Score 2017;  DB 1;  Length 387;
  Best Local Similarity   99.5%;  Pred. No. 3.7e-113;
  Matches  385;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
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Db       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60

Qy      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVMLCT 120

Qy     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
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Db     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180

Qy     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
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Db     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240

Qy     241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300
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Db     241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300

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Db     301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360

Qy     361 SALNPVIYTVFNAEFRNVFRKALRACC 387
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Db     361 SALNRVIYTVFNAEFRNVFRKALRACC 387


RESULT   8
US-08-333-977-17
; Sequence 17, Application US/08333977
; Patent No. 5594108
;  GENERAL INFORMATION:
;    APPLICANT:  Van Tol, Hubert H.M.
;    APPLICANT:  Civelli, Olivier
;    TITLE OF INVENTION:  A No. 5594108el Human Dopamine Receptor and Uses
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Allegretti & Witcoff, Ltd.
;      STREET:  10 South Wacker Drive, Suite 3000
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/333,977
;      FILING DATE:  03-NOV-1994
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/626,618
;      FILING DATE:  7 DEC 1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5594108nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  90,1092
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-715-1000
;      TELEFAX:  312-715-1234
;      TELEX:  810-221-8317
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  387 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
US-08-333-977-17


  Query Match             99.3%;  Score 2017;  DB 1;  Length 387;
  Best Local Similarity   99.5%;  Pred. No. 3.7e-113;
  Matches  385;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60

Qy      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVMLCT 120

Qy     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
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Db     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180

Qy     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
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Db     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240

Qy     241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300
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Db     241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300

Qy     301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360
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Db     301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360

Qy     361 SALNPVIYTVFNAEFRNVFRKALRACC 387
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Db     361 SALNRVIYTVFNAEFRNVFRKALRACC 387


RESULT   9
US-08-056-051-2
; Sequence 2, Application US/08056051
; Patent No. 5516683
;  GENERAL INFORMATION:
;    APPLICANT:  Grandy, David K
;    APPLICANT:  Bunzow, James R
;    APPLICANT:  Civelli, Olivier
;    APPLICANT:  Van Tol, Hubert H.-M.
;    TITLE OF INVENTION:  A No. 5516683el Human Dopamine Receptor and Uses
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Allegretti & Witcoff, Ltd.
;      STREET:  10 South Wacker Drive, Suite 3000
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/056,051
;      FILING DATE:  19930429
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5516683nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  90,1092-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-715-1000
;      TELEFAX:  312-715-1234
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;      TELEX:  910-221-5317
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  387 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-056-051-2


  Query Match             99.0%;  Score 2011;  DB 1;  Length 387;
  Best Local Similarity   99.2%;  Pred. No. 8.5e-113;
  Matches  384;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db      1 MGNRSTADADGLLAGRGRAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60

Qy     61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db     61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVMLCT 120

Qy    121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180

Qy    181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240

Qy    241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300

Qy    301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360
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Db    301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360

Qy    361 SALNPVIYTVFNAEFRNVFRKALRACC 387
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Db    361 SALTPVIYTVFNAEFRNVFRKALRACC 387


RESULT  10
US-07-928-611-18
; Sequence 18, Application US/07928611
; Patent No. 5569601
;  GENERAL INFORMATION:
;    APPLICANT:  Van Tol, Hubert H.M.
;    APPLICANT:  Civelli, Olivier
;    TITLE OF INVENTION:  A No. 5569601el Human Dopamine Receptor and Uses
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Allegretti & Witcoff, Ltd.
;      STREET:  10 South Wacker Drive, Suite 3000
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/928,611
;      FILING DATE:  19920810
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5569601nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  90,1092-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-715-1000
;      TELEFAX:  312-715-1234
;      TELEX:  810-221-8317
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  387 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-928-611-18


  Query Match             99.0%;  Score 2011;  DB 1;  Length 387;
  Best Local Similarity   99.2%;  Pred. No. 8.5e-113;
  Matches  384;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db      1 MGNRSTADADGLLAGRGRAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60

Qy     61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db     61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVMLCT 120

Qy    121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180

Qy    181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240

Qy    241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300

Qy    301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360

Qy    361 SALNPVIYTVFNAEFRNVFRKALRACC 387
          ||| |||||||||||||||||||||||
Db    361 SALTPVIYTVFNAEFRNVFRKALRACC 387


RESULT  11
US-08-487-811A-18
; Sequence 18, Application US/08487811A
; Patent No. 5883226
;  GENERAL INFORMATION:
;    APPLICANT:  Civelli, Olivier
;    APPLICANT:  Van Tol, Hubert H.M.
;    TITLE OF INVENTION:  A No. 5883226el Human Dopamine Receptor and Uses
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McDonnell Boehnen Hulbert & Berghoff
;      STREET:  300 South Wacker Drive
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,811A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5883226nan, Kevin E
;      REGISTRATION NUMBER:  35,303
```

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;      REFERENCE/DOCKET NUMBER:  90,1092-L
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-913-0001
;      TELEFAX:  312-913-0002
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  387 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-487-811A-18


  Query Match            99.0%;  Score 2011;  DB 2;  Length 387;
  Best Local Similarity  99.2%;  Pred. No. 8.5e-113;
  Matches  384;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
           |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db       1 MGNRSTADADGLLAGRGRAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60

Qy      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVMLCT 120

Qy     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180

Qy     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240

Qy     241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300

Qy     301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360

Qy     361 SALNPVIYTVFNAEFRNVFRKALRACC 387
           ||| |||||||||||||||||||||||
Db     361 SALTPVIYTVFNAEFRNVFRKALRACC 387


RESULT  12
US-09-060-694-18
; Sequence 18, Application US/09060694
; Patent No. 6203998
;  GENERAL INFORMATION:
;    APPLICANT:  Civelli, Olivier
;    APPLICANT:  Van Tol, Hubert H.M.
;    TITLE OF INVENTION:  A No. 6203998el Human Dopamine Receptor and Uses
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McDonnell Boehnen Hulbert & Berghoff
;      STREET:  300 South Wacker Drive
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/060,694
;      FILING DATE:  15-APR-1998
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6203998nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  90,1092-MM
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-913-0001
;      TELEFAX:  312-913-0002
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  387 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-060-694-18


  Query Match            99.0%;  Score 2011;  DB 4;  Length 387;
  Best Local Similarity  99.2%;  Pred. No. 8.5e-113;
  Matches  384;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
           |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db       1 MGNRSTADADGLLAGRGRAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60

Qy      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVMLCT 120

Qy     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180

Qy     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240

Qy     241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300

Qy     301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360

Qy     361 SALNPVIYTVFNAEFRNVFRKALRACC 387
           ||| |||||||||||||||||||||||
Db     361 SALTPVIYTVFNAEFRNVFRKALRACC 387


RESULT  13
PCT-US93-07370-18
; Sequence 18, Application PC/TUS9307370
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  A Novel Human Dopamine Receptor and Uses
;    NUMBER OF SEQUENCES:  22
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/07370
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  387 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US93-07370-18


  Query Match            99.0%;  Score 2011;  DB 5;  Length 387;
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  Best Local Similarity   99.2%;  Pred. No. 8.5e-113;
  Matches  384;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       1 MGNRSTADADGLLAGRGRAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60

Qy      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVMLCT 120

Qy     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180

Qy     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240

Qy     241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPPDPCGSNCAPPDAVRAAALPPQTPPQTRRR 300

Qy     301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 RRAKITGRERKAMRVLPVVVGAFLLCWTPFFVVHITQALCPACSVPPRLVSAVTWLGYVN 360

Qy     361 SALNPVIYTVFNAEFRNVFRKALRACC 387
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Db     361 SALTPVIYTVFNAEFRNVFRKALRACC 387


RESULT  14
US-08-056-051-4
; Sequence 4, Application US/08056051
; Patent No. 5516683
;  GENERAL INFORMATION:
;    APPLICANT:  Grandy, David K
;    APPLICANT:  Bunzow, James R
;    APPLICANT:  Civelli, Olivier
;    APPLICANT:  Van Tol, Hubert H.-M.
;    TITLE OF INVENTION:  A No. 5516683el Human Dopamine Receptor and Uses
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Allegretti & Witcoff, Ltd.
;      STREET:  10 South Wacker Drive, Suite 3000
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/056,051
;      FILING DATE:  19930429
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5516683nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  90,1092-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-715-1000
;      TELEFAX:  312-715-1234
;      TELEX:  910-221-5317
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  419 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
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US-08-056-051-4

  Query Match           97.7%;  Score 1985;  DB 1;  Length 419;
  Best Local Similarity   91.6%;  Pred. No. 3.2e-111;
  Matches  384;  Conservative    0;  Mismatches    3;  Indels   32;  Gaps    1;

Qy       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       1 MGNRSTADADGLLAGRGRAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60

Qy      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVMLCT 120

Qy     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180

Qy     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240

Qy     241 PGPPSPTPPAPR--------------------------------LPQDPCGPDCAPPAPG 268
           ||||||||||||                                ||||||||||||||||
Db     241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPRGPCGPDCAPAAPSLPQDPCGPDCAPPAPG 300

Qy     269 LPPDPCGSNCAPPDAVRAAALPPQTPPQTRRRRRAKITGRERKAMRVLPVVVGAFLLCWT 328
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LPPDPCGSNCAPPDAVRAAALPPQTPPQTRRRRRAKITGRERKAMRVLPVVVGAFLLCWT 360

Qy     329 PFFVVHITQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKALRACC 387
           ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db     361 PFFVVHITQALCPACSVPPRLVSAVTWLGYVNSALTPVIYTVFNAEFRNVFRKALRACC 419


RESULT  15
US-07-928-611-20
; Sequence 20, Application US/07928611
; Patent No. 5569601
;  GENERAL INFORMATION:
;    APPLICANT:  Van Tol, Hubert H.M.
;    APPLICANT:  Civelli, Olivier
;    TITLE OF INVENTION:  A No. 5569601el Human Dopamine Receptor and Uses
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Allegretti & Witcoff, Ltd.
;      STREET:  10 South Wacker Drive, Suite 3000
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/928,611
;      FILING DATE:  19920810
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5569601nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  90,1092-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-715-1000
;      TELEFAX:  312-715-1234
;      TELEX:  810-221-8317
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  419 amino acids
;      TYPE:  AMINO ACID
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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-928-611-20


  Query Match             97.7%;  Score 1985;  DB 1;  Length 419;
  Best Local Similarity   91.6%;  Pred. No. 3.2e-111;
  Matches  384;  Conservative    0;  Mismatches    3;  Indels   32;  Gaps    1;

Qy       1 MGNRSTADADGLLAGRGPAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60
           |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db       1 MGNRSTADADGLLAGRGRAAGASAGASAGLAGQGAAALVGGVLLIGAVLAGNSLVCVSVA 60

Qy      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVALCT 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      61 TERALQTPTNSFIVSLAAADLLLALLVLPLFVYSEVQGGAWLLSPRLCDALMAMDVMLCT 120

Qy     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ASIFNLCAISVDRFVAVAVPLRYNRQGGSRRQLLLIGATWLLSAAVAAPVLCGLNDVRGR 180

Qy     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DPAVCRLEDRDYVVYSSVCSFFLPCPLMLLLYWATFRGLQRWEVARRAKLHGRAPRRPSG 240

Qy     241 PGPPSPTPPAPR------------------------------LPQDPCGPDCAPPAPG 268
           ||||||||||||                              ||||||||||||||||
Db     241 PGPPSPTPPAPRLPQDPCGPDCAPPAPGLPRGPCGPDCAPAAPSLPQDPCGPDCAPPAPG 300

Qy     269 LPPDPCGSNCAPPDAVRAAALPPQTPPQTRRRRRAKITGRERKAMRVLPVVVGAFLLCWT 328
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LPPDPCGSNCAPPDAVRAAALPPQTPPQTRRRRRAKITGRERKAMRVLPVVVGAFLLCWT 360

Qy     329 PFFVVHITQALCPACSVPPRLVSAVTWLGYVNSALNPVIYTVFNAEFRNVFRKALRACC 387
           |||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     361 PFFVVHITQALCPACSVPPRLVSAVTWLGYVNSALTPVIYTVFNAEFRNVFRKALRACC 419


Search completed: February 13, 2002, 17:39:13
Job time: 119 sec
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